Full wwPDB EM Validation Report (i)

Sep 28, 2024 – 01:43 PM EDT

PDB ID	:	7KJ4
EMDB ID	:	EMD-22893
Title	:	SARS-CoV-2 Spike Glycoprotein with three ACE2 Bound
Authors	:	Zhang, J.; Xiao, T.S.; Cai, Y.F.; Chen, B.
Deposited on	:	2020-10-25
Resolution	:	3.40 Å(reported)
Based on initial models	:	6M17, 6VYB

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

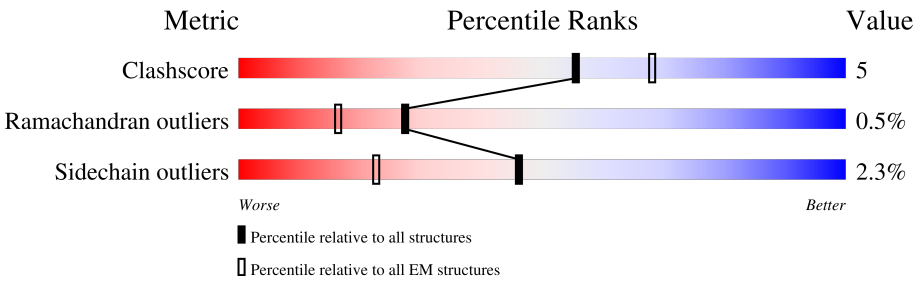
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1234	5% 73% 6% • 21%
1	B	1234	74% 5% 21%
1	C	1234	74% 5% • 21%
2	D	615	• 89% 7% • •
2	E	615	15% 89% 7% • •
2	F	615	88% 88% 7% • •
3	G	2	100%
3	H	2	50% 50%

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Mol	Chain	Length	Quality of chain
3	I	2	100%
3	J	2	100%
3	K	2	100%
3	L	2	100%
3	M	2	100%
3	N	2	100%
3	O	2	50% 50%
3	P	2	50% 100%
3	Q	2	50% 50%
3	R	2	50% 100%
3	S	2	50% 50% 50%
3	T	2	100%
3	U	2	100% 50% 50%
3	V	2	50% 100%
3	W	2	100%
3	X	2	100% 100%
3	Y	2	100% 50% 50%
3	Z	2	100% 50% 50%
3	a	2	100% 50% 50%
3	b	2	100% 100%
3	c	2	100% 50% 50%
3	d	2	100% 50% 50%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 38776 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	981	7658	4890	1269	1464	35	0	0
1	B	981	7665	4893	1271	1466	35	0	0
1	C	981	7661	4891	1271	1464	35	0	0

There are 135 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	conflict	UNP P0DTC2
A	683	GLY	ARG	conflict	UNP P0DTC2
A	684	SER	ALA	conflict	UNP P0DTC2
A	685	GLY	ARG	conflict	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1209	GLY	-	expression tag	UNP P0DTC2
A	1210	SER	-	expression tag	UNP P0DTC2
A	1211	GLY	-	expression tag	UNP P0DTC2
A	1212	GLY	-	expression tag	UNP P0DTC2
A	1213	TYR	-	expression tag	UNP P0DTC2
A	1214	ILE	-	expression tag	UNP P0DTC2
A	1215	PRO	-	expression tag	UNP P0DTC2
A	1216	GLU	-	expression tag	UNP P0DTC2
A	1217	ALA	-	expression tag	UNP P0DTC2
A	1218	PRO	-	expression tag	UNP P0DTC2
A	1219	ARG	-	expression tag	UNP P0DTC2
A	1220	ASP	-	expression tag	UNP P0DTC2
A	1221	GLY	-	expression tag	UNP P0DTC2
A	1222	GLN	-	expression tag	UNP P0DTC2
A	1223	ALA	-	expression tag	UNP P0DTC2
A	1224	TYR	-	expression tag	UNP P0DTC2
A	1225	VAL	-	expression tag	UNP P0DTC2
A	1226	ARG	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1227	LYS	-	expression tag	UNP P0DTC2
A	1228	ASP	-	expression tag	UNP P0DTC2
A	1229	GLY	-	expression tag	UNP P0DTC2
A	1230	GLU	-	expression tag	UNP P0DTC2
A	1231	TRP	-	expression tag	UNP P0DTC2
A	1232	VAL	-	expression tag	UNP P0DTC2
A	1233	LEU	-	expression tag	UNP P0DTC2
A	1234	LEU	-	expression tag	UNP P0DTC2
A	1235	SER	-	expression tag	UNP P0DTC2
A	1236	THR	-	expression tag	UNP P0DTC2
A	1237	PHE	-	expression tag	UNP P0DTC2
A	1238	LEU	-	expression tag	UNP P0DTC2
A	1239	GLY	-	expression tag	UNP P0DTC2
A	1240	GLY	-	expression tag	UNP P0DTC2
A	1241	SER	-	expression tag	UNP P0DTC2
A	1242	HIS	-	expression tag	UNP P0DTC2
A	1243	HIS	-	expression tag	UNP P0DTC2
A	1244	HIS	-	expression tag	UNP P0DTC2
A	1245	HIS	-	expression tag	UNP P0DTC2
A	1246	HIS	-	expression tag	UNP P0DTC2
A	1247	HIS	-	expression tag	UNP P0DTC2
B	682	GLY	ARG	conflict	UNP P0DTC2
B	683	GLY	ARG	conflict	UNP P0DTC2
B	684	SER	ALA	conflict	UNP P0DTC2
B	685	GLY	ARG	conflict	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1209	GLY	-	expression tag	UNP P0DTC2
B	1210	SER	-	expression tag	UNP P0DTC2
B	1211	GLY	-	expression tag	UNP P0DTC2
B	1212	GLY	-	expression tag	UNP P0DTC2
B	1213	TYR	-	expression tag	UNP P0DTC2
B	1214	ILE	-	expression tag	UNP P0DTC2
B	1215	PRO	-	expression tag	UNP P0DTC2
B	1216	GLU	-	expression tag	UNP P0DTC2
B	1217	ALA	-	expression tag	UNP P0DTC2
B	1218	PRO	-	expression tag	UNP P0DTC2
B	1219	ARG	-	expression tag	UNP P0DTC2
B	1220	ASP	-	expression tag	UNP P0DTC2
B	1221	GLY	-	expression tag	UNP P0DTC2
B	1222	GLN	-	expression tag	UNP P0DTC2
B	1223	ALA	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1224	TYR	-	expression tag	UNP P0DTC2
B	1225	VAL	-	expression tag	UNP P0DTC2
B	1226	ARG	-	expression tag	UNP P0DTC2
B	1227	LYS	-	expression tag	UNP P0DTC2
B	1228	ASP	-	expression tag	UNP P0DTC2
B	1229	GLY	-	expression tag	UNP P0DTC2
B	1230	GLU	-	expression tag	UNP P0DTC2
B	1231	TRP	-	expression tag	UNP P0DTC2
B	1232	VAL	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	LEU	-	expression tag	UNP P0DTC2
B	1235	SER	-	expression tag	UNP P0DTC2
B	1236	THR	-	expression tag	UNP P0DTC2
B	1237	PHE	-	expression tag	UNP P0DTC2
B	1238	LEU	-	expression tag	UNP P0DTC2
B	1239	GLY	-	expression tag	UNP P0DTC2
B	1240	GLY	-	expression tag	UNP P0DTC2
B	1241	SER	-	expression tag	UNP P0DTC2
B	1242	HIS	-	expression tag	UNP P0DTC2
B	1243	HIS	-	expression tag	UNP P0DTC2
B	1244	HIS	-	expression tag	UNP P0DTC2
B	1245	HIS	-	expression tag	UNP P0DTC2
B	1246	HIS	-	expression tag	UNP P0DTC2
B	1247	HIS	-	expression tag	UNP P0DTC2
C	682	GLY	ARG	conflict	UNP P0DTC2
C	683	GLY	ARG	conflict	UNP P0DTC2
C	684	SER	ALA	conflict	UNP P0DTC2
C	685	GLY	ARG	conflict	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1209	GLY	-	expression tag	UNP P0DTC2
C	1210	SER	-	expression tag	UNP P0DTC2
C	1211	GLY	-	expression tag	UNP P0DTC2
C	1212	GLY	-	expression tag	UNP P0DTC2
C	1213	TYR	-	expression tag	UNP P0DTC2
C	1214	ILE	-	expression tag	UNP P0DTC2
C	1215	PRO	-	expression tag	UNP P0DTC2
C	1216	GLU	-	expression tag	UNP P0DTC2
C	1217	ALA	-	expression tag	UNP P0DTC2
C	1218	PRO	-	expression tag	UNP P0DTC2
C	1219	ARG	-	expression tag	UNP P0DTC2
C	1220	ASP	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1221	GLY	-	expression tag	UNP P0DTC2
C	1222	GLN	-	expression tag	UNP P0DTC2
C	1223	ALA	-	expression tag	UNP P0DTC2
C	1224	TYR	-	expression tag	UNP P0DTC2
C	1225	VAL	-	expression tag	UNP P0DTC2
C	1226	ARG	-	expression tag	UNP P0DTC2
C	1227	LYS	-	expression tag	UNP P0DTC2
C	1228	ASP	-	expression tag	UNP P0DTC2
C	1229	GLY	-	expression tag	UNP P0DTC2
C	1230	GLU	-	expression tag	UNP P0DTC2
C	1231	TRP	-	expression tag	UNP P0DTC2
C	1232	VAL	-	expression tag	UNP P0DTC2
C	1233	LEU	-	expression tag	UNP P0DTC2
C	1234	LEU	-	expression tag	UNP P0DTC2
C	1235	SER	-	expression tag	UNP P0DTC2
C	1236	THR	-	expression tag	UNP P0DTC2
C	1237	PHE	-	expression tag	UNP P0DTC2
C	1238	LEU	-	expression tag	UNP P0DTC2
C	1239	GLY	-	expression tag	UNP P0DTC2
C	1240	GLY	-	expression tag	UNP P0DTC2
C	1241	SER	-	expression tag	UNP P0DTC2
C	1242	HIS	-	expression tag	UNP P0DTC2
C	1243	HIS	-	expression tag	UNP P0DTC2
C	1244	HIS	-	expression tag	UNP P0DTC2
C	1245	HIS	-	expression tag	UNP P0DTC2
C	1246	HIS	-	expression tag	UNP P0DTC2
C	1247	HIS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called Angiotensin-converting enzyme 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	593	4844	3101	802	912	29	0	0
			Total	C	N	O	S		
2	E	593	4844	3101	802	912	29	0	0
			Total	C	N	O	S		
2	F	593	4844	3101	802	912	29	0	0

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	616	SER	-	expression tag	UNP Q9BYF1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	617	GLY	-	expression tag	UNP Q9BYF1
D	618	GLY	-	expression tag	UNP Q9BYF1
D	619	SER	-	expression tag	UNP Q9BYF1
D	620	HIS	-	expression tag	UNP Q9BYF1
D	621	HIS	-	expression tag	UNP Q9BYF1
D	622	HIS	-	expression tag	UNP Q9BYF1
D	623	HIS	-	expression tag	UNP Q9BYF1
D	624	HIS	-	expression tag	UNP Q9BYF1
D	625	HIS	-	expression tag	UNP Q9BYF1
E	616	SER	-	expression tag	UNP Q9BYF1
E	617	GLY	-	expression tag	UNP Q9BYF1
E	618	GLY	-	expression tag	UNP Q9BYF1
E	619	SER	-	expression tag	UNP Q9BYF1
E	620	HIS	-	expression tag	UNP Q9BYF1
E	621	HIS	-	expression tag	UNP Q9BYF1
E	622	HIS	-	expression tag	UNP Q9BYF1
E	623	HIS	-	expression tag	UNP Q9BYF1
E	624	HIS	-	expression tag	UNP Q9BYF1
E	625	HIS	-	expression tag	UNP Q9BYF1
F	616	SER	-	expression tag	UNP Q9BYF1
F	617	GLY	-	expression tag	UNP Q9BYF1
F	618	GLY	-	expression tag	UNP Q9BYF1
F	619	SER	-	expression tag	UNP Q9BYF1
F	620	HIS	-	expression tag	UNP Q9BYF1
F	621	HIS	-	expression tag	UNP Q9BYF1
F	622	HIS	-	expression tag	UNP Q9BYF1
F	623	HIS	-	expression tag	UNP Q9BYF1
F	624	HIS	-	expression tag	UNP Q9BYF1
F	625	HIS	-	expression tag	UNP Q9BYF1

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	G	2	28	16	2	10	0	0
			Total	C	N	O		
3	H	2	28	16	2	10	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	I	2	28	16	2	10	0	0
3	J	2	28	16	2	10	0	0
3	K	2	28	16	2	10	0	0
3	L	2	28	16	2	10	0	0
3	M	2	28	16	2	10	0	0
3	N	2	28	16	2	10	0	0
3	O	2	28	16	2	10	0	0
3	P	2	28	16	2	10	0	0
3	Q	2	28	16	2	10	0	0
3	R	2	28	16	2	10	0	0
3	S	2	28	16	2	10	0	0
3	T	2	28	16	2	10	0	0
3	U	2	28	16	2	10	0	0
3	V	2	28	16	2	10	0	0
3	W	2	28	16	2	10	0	0
3	X	2	28	16	2	10	0	0
3	Y	2	28	16	2	10	0	0
3	Z	2	28	16	2	10	0	0
3	a	2	28	16	2	10	0	0
3	b	2	28	16	2	10	0	0
3	c	2	28	16	2	10	0	0

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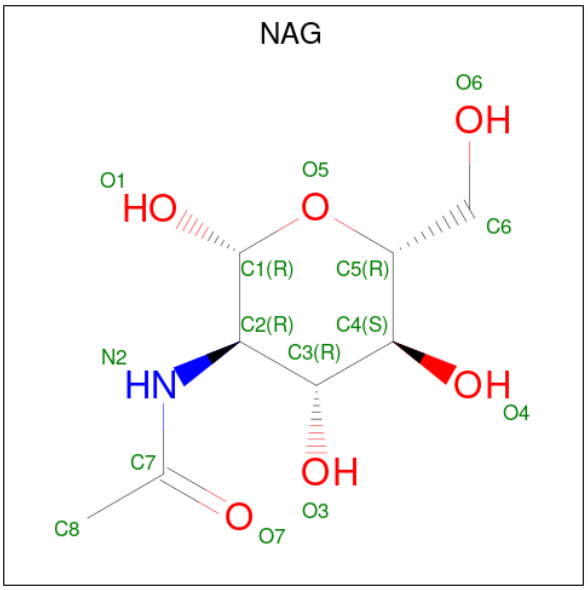
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	d	2	28	16	2	10	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	A	1	14	8	1	5	0
4	A	1	14	8	1	5	0
4	A	1	14	8	1	5	0
4	A	1	14	8	1	5	0
4	A	1	14	8	1	5	0
4	A	1	14	8	1	5	0
4	A	1	14	8	1	5	0
4	A	1	14	8	1	5	0
4	A	1	14	8	1	5	0
4	A	1	14	8	1	5	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	A	1	14	8	1	5	0
			Total	C	N	O	
4	A	1	14	8	1	5	0
			Total	C	N	O	
4	A	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	B	1	14	8	1	5	0
			Total	C	N	O	
4	C	1	14	8	1	5	0
			Total	C	N	O	
4	C	1	14	8	1	5	0
			Total	C	N	O	
4	C	1	14	8	1	5	0
			Total	C	N	O	
4	C	1	14	8	1	5	0
			Total	C	N	O	
4	C	1	14	8	1	5	0

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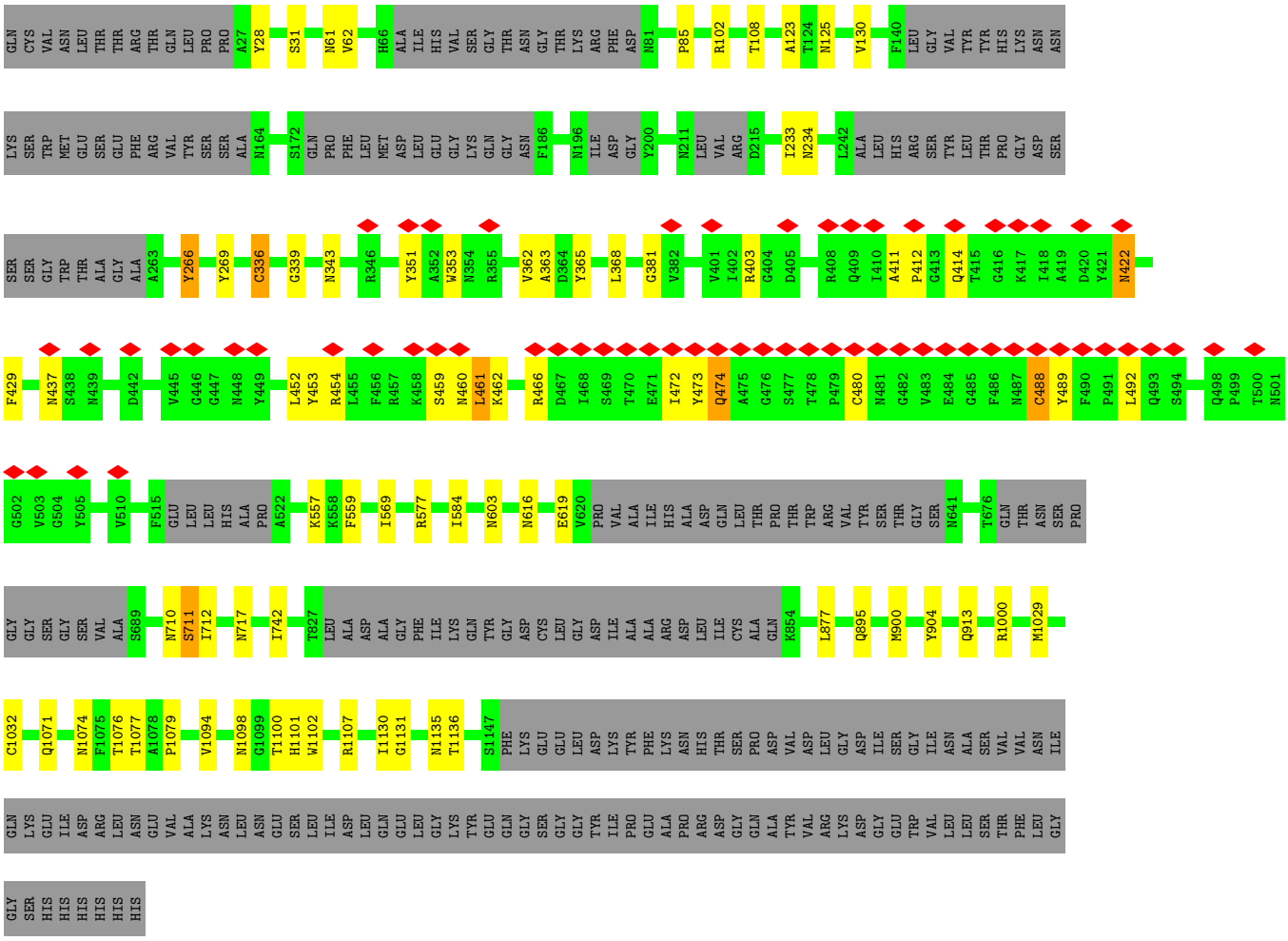
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	C	1	14	8	1	5	0
4	C	1	14	8	1	5	0
4	C	1	14	8	1	5	0
4	C	1	14	8	1	5	0
4	C	1	14	8	1	5	0
4	C	1	14	8	1	5	0
4	C	1	14	8	1	5	0
4	C	1	14	8	1	5	0
4	D	1	14	8	1	5	0
4	E	1	14	8	1	5	0
4	F	1	14	8	1	5	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

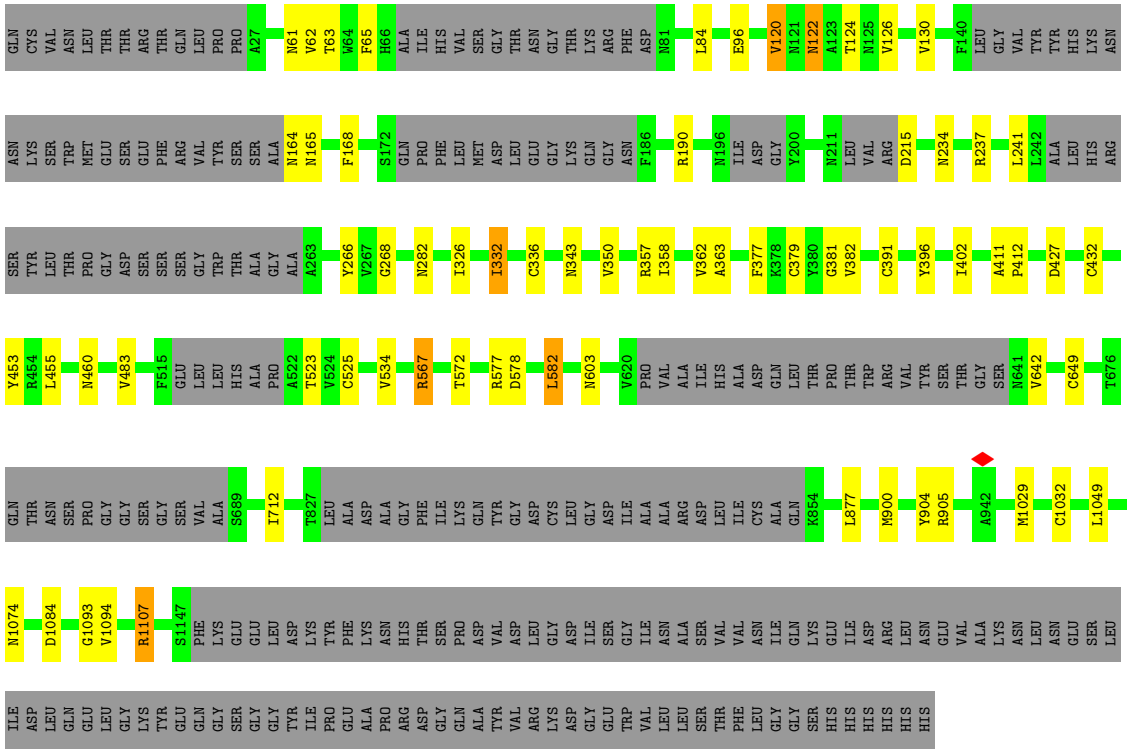
• Molecule 1: Spike glycoprotein

Chain A:



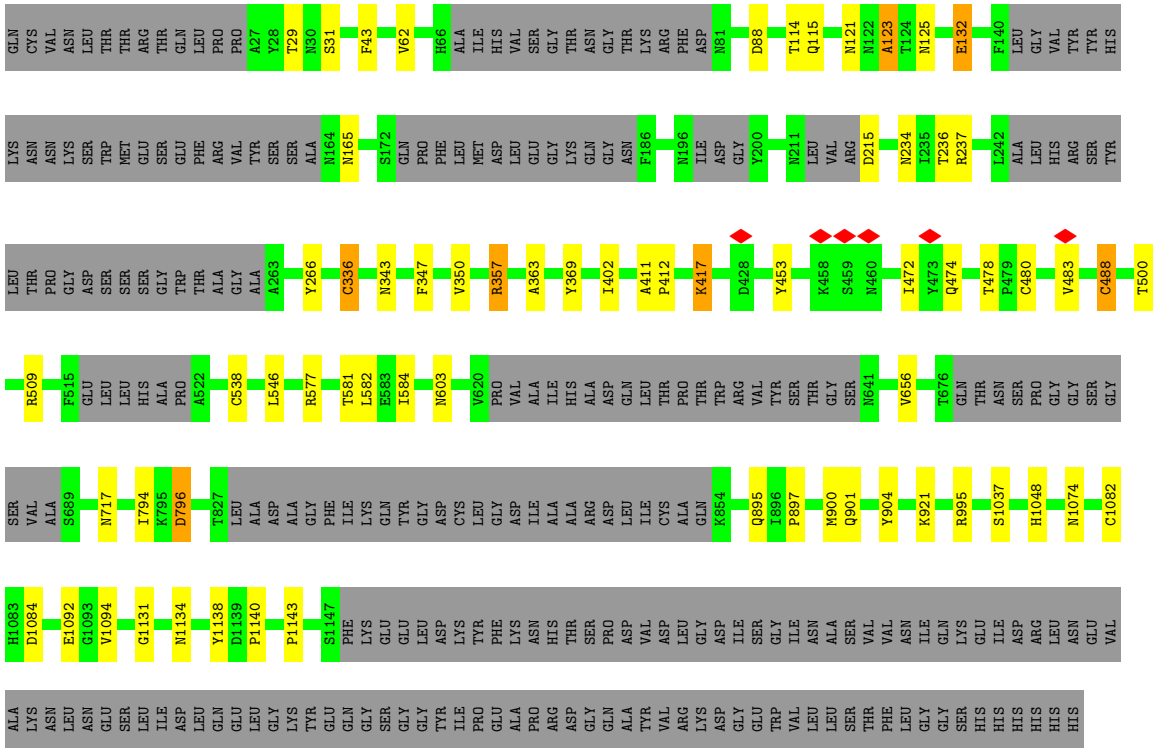
• Molecule 1: Spike glycoprotein

Chain B:



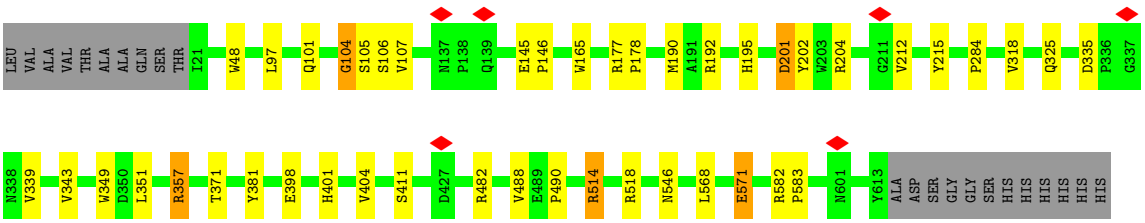
• Molecule 1: Spike glycoprotein

Chain C:



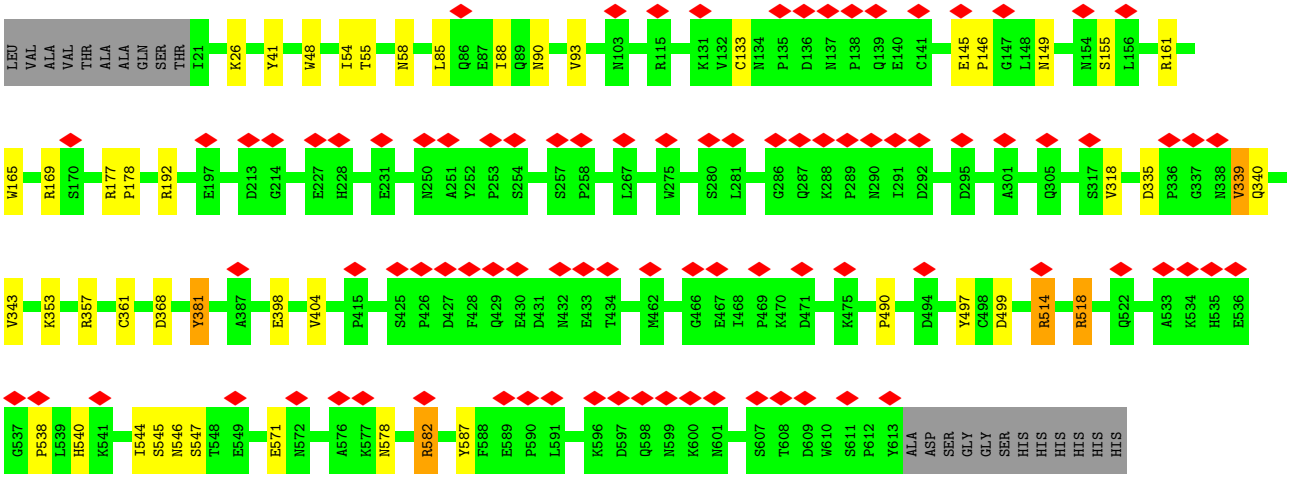
• Molecule 2: Angiotensin-converting enzyme 2

Chain D:



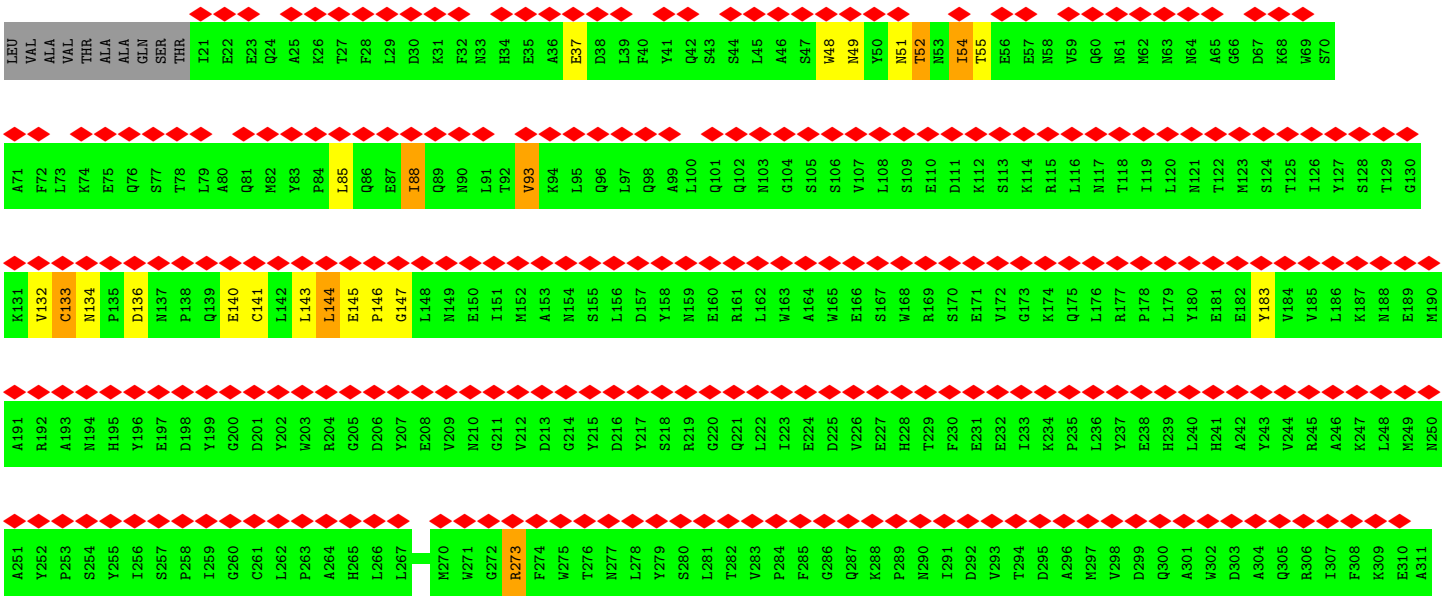
- Molecule 2: Angiotensin-converting enzyme 2

Chain E:



- Molecule 2: Angiotensin-converting enzyme 2

Chain F:



E312 K313 F314 F315 V316 S317 V318 G319 L320 P321 N322 M323 T324 Q325 G326 F327 W328 E329 N330 S331 M332 L333 T334 D335 N338 V339 Q340 K341 A342 V343 C344 H345 A348 G352 K353 G354 D355 F356 R357 I358 L359 M360 C361 T362 K363 V364 T365 M366 D367 D368 F369 L370 T371 A372 M376 G377

H378 I379 Q380 Y381 D382 M383 A384 Y385 A386 A387 Q388 P389 F390 L391 L392 R393 N394 G395 A396 N397 E398 G399 F400 H401 E402 A403 V404 G405 E406 L410 S411 A412 A413 T414 P415 K416 H417 L418 K419 S420 I421 G422 L423 L424 S425 P426 D427 F428 Q429 E430 D431 N432 E433 T434 E435 I436 N437 F438 L439

L440 K441 Q442 A443 L444 T445 I446 V447 G448 T449 L450 P451 F452 T453 Y454 M455 L456 E457 K458 W459 R460 W461 M462 V463 F464 K465 G466 E467 I468 P469 K470 D471 Q472 W473 M474 K475 K476 W477 W478 E479 M480 K481 R482 E483 I484 V485 G486 V487 V488 E489 P490 V491 P492 H493 D494 E495 T496 Y497 C498 D499

P500 A501 S502 L503 F504 H505 V506 S507 N508 D509 Y510 S511 F512 I513 R514 Y515 Y516 T517 R518 T519 L520 Y521 Q522 F523 Q524 E527 A528 L529 C530 Q531 A532 A533 K534 H535 E536 G537 P538 L539 H540 K541 C542 D543 I544 S545 N546 S547 T548 E549 A550 G551 Q552 K553 L554 F555 N556 M557 L558 R559 L560

G561 K562 S563 E564 P565 W566 T567 L568 A569 L570 E571 N572 V573 V574 G575 A576 K577 N578 M579 N580 V581 R582 P583 L584 L585 N586 Y587 F588 E589 P590 L591 F592 T593 W594 L595 K596 D597 Q598 N599 K600 N601 S602 F603 V604 G605 W606 S607 T608 D609 W610 S611 P612 Y613 ALA ASP SER GLY GLY SER HIS

HIS HIS HIS HIS HIS

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 100%

NAG1 NAG2

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H: 50% 50%

NAG1 NAG2

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

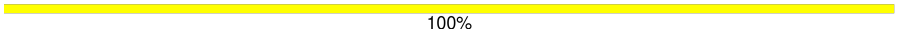
Chain I: 100%

NAG1 NAG2

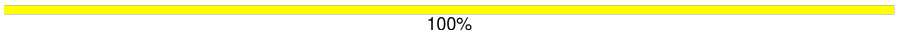
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J: 100%

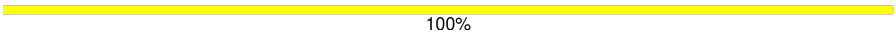
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K: 

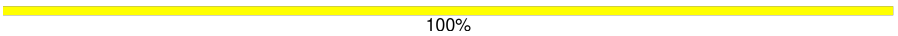
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L: 

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M: 

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N: 

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

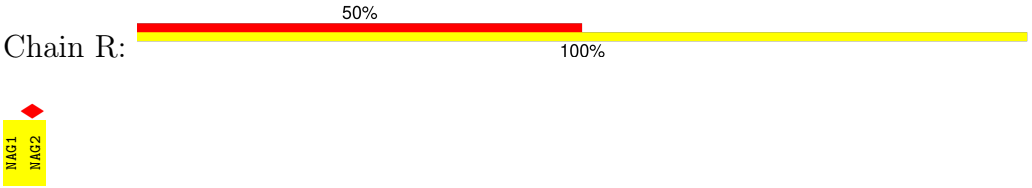
Chain P:

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:

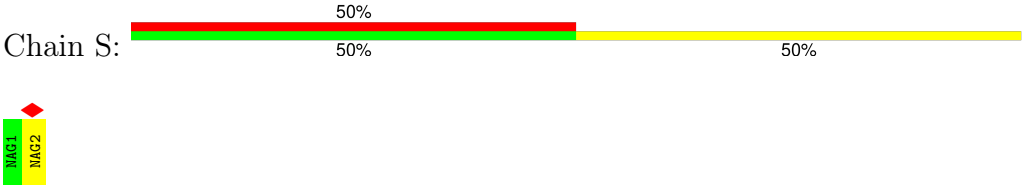
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:



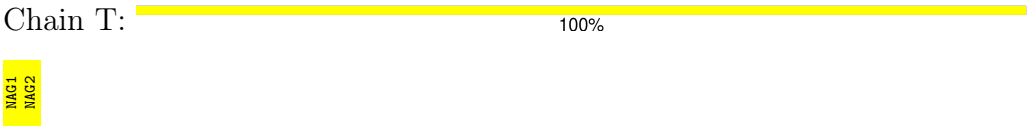
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:



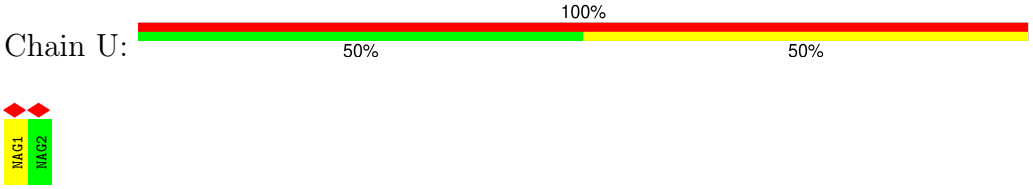
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:



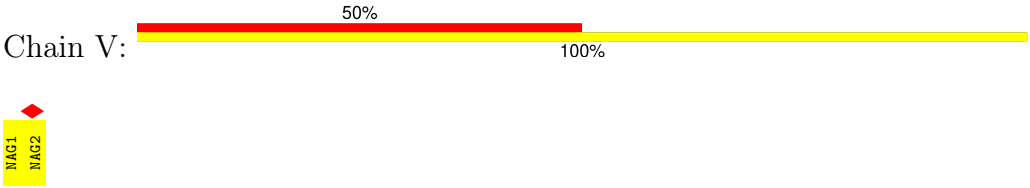
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:



• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain V:



• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W: 100%

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X: 100% 100%

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y: 100% 50% 50%

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z: 100% 50% 50%

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a: 100% 50% 50%

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b: 100% 100%

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain c:

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26298	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50.05	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.084	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	396.0, 396.0, 396.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.62	0/7827	0.92	0/10645
1	B	0.62	0/7834	0.92	0/10654
1	C	0.63	0/7830	0.92	0/10649
2	D	0.66	0/4981	0.94	0/6767
2	E	0.67	0/4981	0.95	0/6767
2	F	0.68	0/4981	0.96	0/6767
All	All	0.64	0/38434	0.93	0/52249

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7658	0	7451	104	0
1	B	7665	0	7464	69	0
1	C	7661	0	7460	74	0
2	D	4844	0	4613	39	0
2	E	4844	0	4617	50	0
2	F	4844	0	4619	43	0
3	G	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	28	0	25	6	0
3	I	28	0	25	0	0
3	J	28	0	25	0	0
3	K	28	0	25	0	0
3	L	28	0	25	0	0
3	M	28	0	25	0	0
3	N	28	0	25	0	0
3	O	28	0	25	4	0
3	P	28	0	25	0	0
3	Q	28	0	25	0	0
3	R	28	0	25	5	0
3	S	28	0	25	0	0
3	T	28	0	25	3	0
3	U	28	0	25	2	0
3	V	28	0	25	3	0
3	W	28	0	25	0	0
3	X	28	0	25	0	0
3	Y	28	0	25	0	0
3	Z	28	0	25	2	0
3	a	28	0	25	0	0
3	b	28	0	25	0	0
3	c	28	0	25	0	0
3	d	28	0	25	0	0
4	A	182	0	169	30	0
4	B	182	0	169	25	0
4	C	182	0	169	20	0
4	D	14	0	13	0	0
4	E	14	0	13	0	0
4	F	14	0	13	2	0
All	All	38776	0	37370	354	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (354) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:ASN:HD21	4:B:1313:NAG:C1	0.97	1.61
1:B:122:ASN:HD21	4:B:1302:NAG:C1	1.13	1.58
1:B:1074:ASN:HD21	4:B:1312:NAG:C1	1.02	1.57
1:A:234:ASN:HD21	4:A:1303:NAG:C1	0.98	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:ASN:HD21	4:B:1304:NAG:C1	0.96	1.55
1:B:61:ASN:HD21	4:B:1301:NAG:C1	0.96	1.53
1:B:343:ASN:ND2	4:B:1306:NAG:C1	1.70	1.53
1:C:717:ASN:ND2	4:C:1311:NAG:C1	1.68	1.52
2:D:546:ASN:ND2	3:T:1:NAG:C1	1.69	1.51
2:F:322:ASN:HD21	4:F:701:NAG:C1	1.25	1.50
1:A:61:ASN:ND2	4:A:1301:NAG:C1	1.68	1.50
1:B:282:ASN:ND2	4:B:1304:NAG:C1	1.75	1.49
1:C:1134:ASN:ND2	3:O:1:NAG:C1	1.79	1.45
1:B:61:ASN:ND2	4:B:1301:NAG:C1	1.76	1.44
1:B:1074:ASN:ND2	4:B:1312:NAG:C1	1.74	1.44
1:A:234:ASN:ND2	4:A:1303:NAG:C1	1.81	1.42
1:B:165:ASN:ND2	4:B:1313:NAG:C1	1.78	1.40
1:C:343:ASN:HD21	4:C:1306:NAG:C1	1.36	1.36
1:A:1074:ASN:HD21	4:A:1312:NAG:C1	1.38	1.35
2:D:215:TYR:CE1	2:D:568:LEU:HD13	1.62	1.34
1:A:1098:ASN:HD21	3:H:1:NAG:C1	1.40	1.34
1:B:122:ASN:ND2	4:B:1302:NAG:C1	1.95	1.27
1:C:165:ASN:ND2	4:C:1313:NAG:C1	1.99	1.25
1:C:343:ASN:ND2	4:C:1306:NAG:C1	1.98	1.25
1:B:603:ASN:HD21	4:B:1307:NAG:C1	1.50	1.24
1:B:603:ASN:ND2	4:B:1307:NAG:C1	1.99	1.24
2:F:322:ASN:ND2	4:F:701:NAG:C1	2.03	1.18
2:F:530:CYS:SG	2:F:535:HIS:HB2	1.83	1.18
1:C:603:ASN:HD21	4:C:1307:NAG:C1	1.61	1.13
1:A:1074:ASN:ND2	4:A:1312:NAG:C1	2.12	1.12
1:A:1098:ASN:ND2	3:H:1:NAG:C1	2.13	1.11
1:A:616:ASN:ND2	4:A:1308:NAG:C1	2.16	1.07
1:A:1102:TRP:HB2	1:A:1135:ASN:HD21	1.21	1.06
1:C:603:ASN:ND2	4:C:1307:NAG:C1	2.20	1.05
1:A:603:ASN:OD1	4:A:1307:NAG:C1	2.06	1.04
1:B:1074:ASN:HD21	4:B:1312:NAG:C2	1.69	1.04
1:C:165:ASN:HD22	4:C:1313:NAG:C1	1.64	1.02
1:C:1074:ASN:ND2	4:C:1312:NAG:C1	2.23	1.00
2:D:582:ARG:HB3	2:D:583:PRO:HD3	1.39	0.99
1:C:115:GLN:NE2	1:C:165:ASN:O	1.96	0.99
1:B:332:ILE:HD11	1:B:362:VAL:HG11	1.44	0.98
1:A:1130:ILE:HD11	1:C:921:LYS:HE3	1.47	0.96
1:A:343:ASN:HD21	4:A:1306:NAG:C1	1.78	0.96
1:C:234:ASN:HD21	4:C:1303:NAG:C1	1.80	0.95
1:C:603:ASN:ND2	4:C:1307:NAG:O5	1.97	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:236:THR:HG21	4:C:1303:NAG:O6	1.67	0.94
1:C:1134:ASN:HD22	3:O:1:NAG:C1	1.64	0.93
1:C:1134:ASN:HD21	3:O:1:NAG:C1	1.57	0.93
1:A:616:ASN:HD22	4:A:1308:NAG:C1	1.82	0.93
2:D:215:TYR:HE1	2:D:568:LEU:HD13	1.27	0.92
1:A:1102:TRP:HB2	1:A:1135:ASN:ND2	1.85	0.92
1:C:165:ASN:HD21	4:C:1313:NAG:C1	1.84	0.91
2:E:540:HIS:HB3	2:E:587:TYR:CE1	2.06	0.90
2:D:215:TYR:CE1	2:D:568:LEU:CD1	2.55	0.89
2:F:530:CYS:SG	2:F:535:HIS:CB	2.61	0.88
2:E:340:GLN:HE22	3:U:1:NAG:H82	1.37	0.88
2:D:105:SER:O	2:D:107:VAL:N	2.07	0.87
1:A:1094:VAL:HG23	1:C:900:MET:HE3	1.55	0.86
1:C:29:THR:O	1:C:62:VAL:HG22	1.75	0.85
1:C:1074:ASN:HD21	4:C:1312:NAG:C1	1.87	0.85
1:A:125:ASN:CB	4:A:1302:NAG:H83	2.06	0.85
2:F:85:LEU:O	2:F:88:ILE:HG12	1.77	0.84
1:B:1074:ASN:ND2	4:B:1312:NAG:C2	2.34	0.84
1:A:1100:THR:CG2	1:A:1101:HIS:CE1	2.62	0.81
2:F:330:ASN:C	2:F:357:ARG:HD3	2.01	0.81
2:D:215:TYR:CZ	2:D:568:LEU:HD13	2.15	0.81
1:A:28:TYR:CD1	4:A:1301:NAG:H81	2.15	0.80
3:R:1:NAG:C3	3:R:2:NAG:HN2	1.95	0.79
2:E:55:THR:CG2	2:E:58:ASN:HD22	1.95	0.79
1:A:603:ASN:HD21	4:A:1307:NAG:C1	1.95	0.79
1:A:616:ASN:HD21	4:A:1308:NAG:C1	1.95	0.78
1:A:125:ASN:CB	4:A:1302:NAG:C8	2.62	0.77
2:E:55:THR:HG23	2:E:58:ASN:H	1.49	0.77
2:D:546:ASN:CG	3:T:1:NAG:C1	2.54	0.77
1:A:603:ASN:ND2	4:A:1307:NAG:C1	2.49	0.76
2:E:538:PRO:HB2	2:E:540:HIS:CE1	2.20	0.76
2:D:351:LEU:HD12	2:D:357:ARG:HH21	1.51	0.76
2:F:403:ALA:HB2	2:F:518:ARG:HG2	1.68	0.75
1:A:900:MET:CE	1:B:1094:VAL:HG23	2.17	0.75
1:A:1100:THR:HG22	1:A:1101:HIS:CE1	2.23	0.74
1:A:913:GLN:OE1	1:B:1107:ARG:NH2	2.20	0.74
1:A:559:PHE:CE1	1:C:43:PHE:CD2	2.75	0.74
1:A:61:ASN:ND2	4:A:1301:NAG:O5	2.21	0.73
1:A:603:ASN:CG	4:A:1307:NAG:C1	2.56	0.73
2:D:351:LEU:CD1	2:D:357:ARG:HH21	2.02	0.73
1:A:904:TYR:CE2	1:B:1107:ARG:HD3	2.24	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:473:TYR:O	1:A:474:GLN:HG2	1.89	0.73
1:C:1074:ASN:HD22	4:C:1312:NAG:C1	2.02	0.72
1:B:1093:GLY:HA2	1:B:1107:ARG:HG2	1.69	0.72
2:E:540:HIS:HA	2:E:587:TYR:HE1	1.54	0.72
1:A:61:ASN:CG	4:A:1301:NAG:C1	2.57	0.72
1:B:453:TYR:OH	1:B:455:LEU:HD13	1.90	0.72
1:A:1100:THR:HG21	1:A:1101:HIS:CE1	2.25	0.72
2:F:48:TRP:O	2:F:52:THR:HG22	1.89	0.71
2:E:340:GLN:NE2	3:U:1:NAG:H82	2.05	0.71
1:C:347:PHE:CE2	1:C:509:ARG:HD3	2.26	0.71
1:A:343:ASN:ND2	4:A:1306:NAG:C1	2.54	0.71
2:D:398:GLU:HG3	2:D:514:ARG:HB3	1.72	0.71
2:E:540:HIS:HB3	2:E:587:TYR:CZ	2.26	0.69
2:F:85:LEU:O	2:F:88:ILE:CG1	2.40	0.69
2:D:105:SER:C	2:D:107:VAL:H	1.95	0.69
1:B:1074:ASN:ND2	4:B:1312:NAG:N2	2.40	0.69
2:E:339:VAL:HG12	2:E:339:VAL:O	1.92	0.68
2:E:540:HIS:CB	2:E:587:TYR:CE1	2.76	0.68
2:D:48:TRP:CZ3	2:D:357:ARG:HD2	2.28	0.68
1:A:1094:VAL:HG23	1:C:900:MET:CE	2.22	0.68
2:E:318:VAL:O	2:E:547:SER:O	2.11	0.68
1:A:559:PHE:CE1	1:C:43:PHE:CE2	2.82	0.68
1:A:616:ASN:HD21	4:A:1308:NAG:C2	2.06	0.67
1:A:559:PHE:CD1	1:C:43:PHE:CD1	2.82	0.67
1:A:900:MET:HE2	1:B:1094:VAL:HG23	1.75	0.67
1:B:120:VAL:HG13	1:B:241:LEU:HD12	1.75	0.67
2:E:85:LEU:HD12	2:E:88:ILE:HG13	1.78	0.65
2:D:582:ARG:CB	2:D:583:PRO:HD3	2.19	0.65
2:D:105:SER:O	2:D:107:VAL:HG22	1.96	0.64
2:D:192:ARG:O	2:D:195:HIS:N	2.25	0.64
1:C:417:LYS:HB3	1:C:453:TYR:OH	1.97	0.64
1:B:234:ASN:ND2	4:B:1303:NAG:C1	2.61	0.64
2:E:55:THR:HG22	2:E:58:ASN:HD22	1.62	0.64
2:F:273:ARG:HG3	2:F:452:PHE:CE2	2.33	0.64
2:D:215:TYR:HE1	2:D:568:LEU:CD1	2.01	0.64
1:C:343:ASN:CG	4:C:1306:NAG:C1	2.66	0.63
1:A:368:LEU:HD23	4:A:1306:NAG:H83	1.80	0.63
1:B:411:ALA:HB1	1:B:412:PRO:HD2	1.78	0.63
1:A:1130:ILE:HD11	1:C:921:LYS:CE	2.26	0.63
2:E:518:ARG:HD2	2:E:518:ARG:C	2.18	0.63
2:E:41:TYR:CD1	2:E:353:LYS:CG	2.82	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:1:NAG:H3	3:R:2:NAG:HN2	1.64	0.63
1:A:616:ASN:HD21	4:A:1308:NAG:H2	1.62	0.63
2:D:48:TRP:CE3	2:D:357:ARG:HD2	2.34	0.62
2:E:26:LYS:HE2	3:V:1:NAG:HN2	1.64	0.62
1:A:31:SER:HB3	1:A:62:VAL:HG23	1.82	0.62
2:E:85:LEU:O	2:E:88:ILE:HG12	2.00	0.61
2:E:398:GLU:HG3	2:E:514:ARG:HB3	1.82	0.61
2:F:273:ARG:HG3	2:F:452:PHE:CD2	2.36	0.61
1:B:164:ASN:HD22	4:B:1313:NAG:C8	2.14	0.60
2:F:134:ASN:HD21	2:F:136:ASP:HB2	1.66	0.60
2:F:582:ARG:CB	2:F:583:PRO:HD3	2.31	0.60
1:A:123:ALA:C	1:A:125:ASN:H	2.05	0.60
1:B:215:ASP:N	1:B:266:TYR:HH	2.00	0.60
1:C:215:ASP:N	1:C:266:TYR:HH	1.98	0.60
1:A:31:SER:HB3	1:A:62:VAL:CG2	2.31	0.60
1:B:234:ASN:HD21	4:B:1303:NAG:C1	2.14	0.60
1:B:332:ILE:HG23	1:B:332:ILE:O	2.02	0.59
1:A:1074:ASN:HD21	4:A:1312:NAG:C2	2.14	0.59
2:E:90:ASN:HB3	2:E:93:VAL:HG12	1.84	0.59
2:D:104:GLY:O	2:D:190:MET:HG2	2.01	0.59
2:F:145:GLU:N	2:F:146:PRO:HD2	2.18	0.59
2:E:540:HIS:HA	2:E:587:TYR:CE1	2.37	0.58
1:C:411:ALA:HB1	1:C:412:PRO:HD2	1.84	0.58
2:F:381:TYR:CE1	2:F:558:LEU:HA	2.39	0.58
1:A:411:ALA:HB1	1:A:412:PRO:HD2	1.85	0.58
2:E:540:HIS:CA	2:E:587:TYR:CE1	2.87	0.58
2:F:143:LEU:HB2	2:F:146:PRO:HG2	1.86	0.57
1:B:1074:ASN:HD22	4:B:1312:NAG:C1	2.06	0.57
1:C:62:VAL:HG23	1:C:62:VAL:O	2.02	0.57
1:A:616:ASN:HB3	1:A:619:GLU:OE1	2.04	0.56
2:F:51:ASN:O	2:F:359:LEU:CD2	2.54	0.56
2:F:340:GLN:NE2	3:Z:1:NAG:H82	2.21	0.56
2:F:582:ARG:HB2	2:F:583:PRO:HD3	1.88	0.56
1:B:63:THR:HG21	1:B:65:PHE:CZ	2.40	0.56
2:F:145:GLU:N	2:F:146:PRO:CD	2.69	0.56
1:B:165:ASN:HA	1:C:357:ARG:HH22	1.71	0.55
1:C:500:THR:HG1	2:E:41:TYR:HH	1.54	0.55
1:C:794:ILE:CG2	1:C:796:ASP:OD2	2.54	0.55
1:A:1094:VAL:CG2	1:C:900:MET:HE3	2.32	0.55
2:D:349:TRP:HB2	2:D:357:ARG:O	2.06	0.55
1:B:120:VAL:CG1	1:B:241:LEU:HD12	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:794:ILE:HG22	1:C:796:ASP:OD2	2.06	0.55
1:A:1102:TRP:CB	1:A:1135:ASN:ND2	2.65	0.55
2:E:169:ARG:HG2	2:E:499:ASP:OD1	2.06	0.55
2:F:340:GLN:HE22	3:Z:1:NAG:H82	1.70	0.55
1:A:62:VAL:CG1	1:A:266:TYR:HB3	2.36	0.55
2:E:177:ARG:HB3	2:E:178:PRO:HD3	1.88	0.55
2:E:544:ILE:HG13	2:E:544:ILE:O	2.07	0.55
1:A:717:ASN:ND2	1:A:1071:GLN:OE1	2.40	0.54
1:B:336:CYS:SG	1:B:363:ALA:HB2	2.48	0.54
1:A:1107:ARG:HD3	1:C:904:TYR:CE2	2.43	0.54
1:A:711:SER:O	1:C:897:PRO:HD3	2.08	0.54
2:E:26:LYS:HE2	3:V:1:NAG:C8	2.38	0.54
2:D:101:GLN:O	2:D:101:GLN:HG2	2.07	0.54
1:A:1100:THR:OG1	3:H:1:NAG:H83	2.08	0.54
1:A:28:TYR:CE1	4:A:1301:NAG:H81	2.42	0.54
1:A:900:MET:HE1	1:B:1094:VAL:HG23	1.86	0.54
2:E:41:TYR:CD1	2:E:353:LYS:HG3	2.43	0.54
2:E:538:PRO:CB	2:E:540:HIS:CE1	2.89	0.53
2:E:55:THR:HG23	2:E:58:ASN:N	2.21	0.53
1:A:557:LYS:HB3	1:A:559:PHE:CE1	2.43	0.53
1:B:120:VAL:HG13	1:B:241:LEU:CD1	2.38	0.53
1:B:336:CYS:SG	1:B:358:ILE:CG2	2.96	0.53
1:C:417:LYS:CG	1:C:453:TYR:OH	2.57	0.53
1:A:559:PHE:CD1	1:C:43:PHE:CG	2.97	0.53
2:D:215:TYR:CD1	2:D:568:LEU:HB2	2.43	0.53
1:A:368:LEU:CD2	4:A:1306:NAG:C8	2.86	0.53
1:B:164:ASN:HD22	4:B:1313:NAG:H82	1.72	0.53
1:A:472:ILE:HG22	1:A:488:CYS:SG	2.49	0.53
1:B:84:LEU:O	1:B:237:ARG:HG2	2.08	0.53
1:A:461:LEU:HD22	1:A:462:LYS:H	1.74	0.53
1:C:1131:GLY:HA2	4:C:1310:NAG:C8	2.39	0.53
2:D:582:ARG:HB3	2:D:583:PRO:CD	2.26	0.53
1:C:350:VAL:HG13	1:C:402:ILE:HD11	1.91	0.53
1:B:343:ASN:CG	4:B:1306:NAG:C1	2.69	0.52
1:B:577:ARG:HD3	1:B:582:LEU:HD22	1.91	0.52
2:E:41:TYR:CD1	2:E:353:LYS:HG2	2.44	0.52
2:D:104:GLY:O	2:D:190:MET:SD	2.67	0.52
1:C:347:PHE:CE2	1:C:509:ARG:CD	2.93	0.52
3:R:1:NAG:H3	3:R:2:NAG:N2	2.25	0.52
1:C:114:THR:C	1:C:132:GLU:HG3	2.30	0.52
1:A:336:CYS:SG	1:A:362:VAL:O	2.68	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:900:MET:CE	1:C:1094:VAL:HG23	2.40	0.51
2:F:133:CYS:HA	2:F:141:CYS:HA	1.91	0.51
1:C:417:LYS:CB	1:C:453:TYR:OH	2.58	0.51
2:D:104:GLY:O	2:D:190:MET:CG	2.58	0.51
1:B:120:VAL:CG1	1:B:241:LEU:CD1	2.89	0.51
2:F:49:ASN:HA	2:F:52:THR:CG2	2.40	0.51
2:E:318:VAL:HB	2:E:544:ILE:O	2.10	0.51
2:F:48:TRP:O	2:F:52:THR:CG2	2.59	0.51
1:A:422:ASN:ND2	1:A:454:ARG:HB2	2.26	0.51
1:A:1101:HIS:CE1	3:H:1:NAG:H3	2.46	0.50
2:F:143:LEU:CB	2:F:146:PRO:HG2	2.41	0.50
1:B:905:ARG:HD2	1:B:1049:LEU:O	2.11	0.50
1:B:164:ASN:ND2	4:B:1313:NAG:C8	2.74	0.50
1:A:717:ASN:HB2	1:A:1071:GLN:HB2	1.93	0.50
1:C:717:ASN:ND2	4:C:1311:NAG:O5	2.39	0.49
2:E:41:TYR:CE1	2:E:353:LYS:HB2	2.47	0.49
1:A:895:GLN:O	1:B:712:ILE:HA	2.12	0.49
2:F:51:ASN:O	2:F:359:LEU:HD22	2.12	0.49
1:A:472:ILE:HG21	1:A:480:CYS:SG	2.52	0.49
1:B:62:VAL:HG12	1:B:268:GLY:HA3	1.95	0.49
2:F:482:ARG:NH2	2:F:488:VAL:HG23	2.28	0.49
1:A:125:ASN:CB	4:A:1302:NAG:H82	2.40	0.49
2:E:55:THR:HG21	2:E:58:ASN:HD22	1.75	0.49
2:E:381:TYR:CD2	2:E:404:VAL:HG11	2.47	0.49
2:F:330:ASN:HB3	2:F:357:ARG:NE	2.27	0.48
1:A:712:ILE:HA	1:C:895:GLN:O	2.12	0.48
1:A:85:PRO:O	1:A:269:TYR:HE1	1.96	0.48
1:A:473:TYR:O	1:A:474:GLN:CG	2.59	0.48
1:B:164:ASN:ND2	4:B:1313:NAG:H83	2.28	0.48
2:D:105:SER:C	2:D:107:VAL:N	2.63	0.48
2:D:398:GLU:CG	2:D:514:ARG:HB3	2.41	0.48
2:F:51:ASN:O	2:F:359:LEU:HD21	2.14	0.48
1:A:577:ARG:HB2	1:A:584:ILE:CD1	2.43	0.48
1:B:120:VAL:O	1:B:126:VAL:HG13	2.13	0.48
2:D:546:ASN:HD22	3:T:1:NAG:C1	2.06	0.48
2:E:26:LYS:HE2	3:V:1:NAG:H82	1.96	0.48
1:B:357:ARG:HG2	1:B:396:TYR:CD1	2.49	0.48
1:A:559:PHE:CD1	1:C:43:PHE:CE1	3.01	0.48
2:F:144:LEU:HG	2:F:145:GLU:N	2.28	0.48
1:A:710:ASN:O	1:A:1077:THR:N	2.40	0.47
3:R:2:NAG:C3	3:R:2:NAG:H83	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:559:PHE:CE1	1:C:43:PHE:CG	3.02	0.47
1:C:472:ILE:HG22	1:C:488:CYS:HB2	1.97	0.47
1:C:478:THR:HG23	1:C:488:CYS:SG	2.54	0.47
1:A:1079:PRO:HD2	1:A:1131:GLY:O	2.15	0.47
2:D:482:ARG:NH2	2:D:488:VAL:HG23	2.29	0.47
2:F:133:CYS:SG	2:F:140:GLU:O	2.72	0.47
1:C:234:ASN:ND2	4:C:1303:NAG:C1	2.64	0.47
2:D:582:ARG:CB	2:D:583:PRO:CD	2.90	0.46
2:F:132:VAL:HG12	2:F:132:VAL:O	2.15	0.46
2:D:145:GLU:HB3	2:D:146:PRO:HD3	1.97	0.46
1:B:326:ILE:HD11	1:B:534:VAL:H	1.80	0.46
1:C:1138:TYR:OH	1:C:1143:PRO:HG2	2.15	0.46
2:F:582:ARG:HA	2:F:582:ARG:HD2	1.54	0.46
1:B:603:ASN:HD22	4:B:1307:NAG:C1	2.15	0.46
1:C:1138:TYR:O	1:C:1140:PRO:HD3	2.16	0.46
2:D:568:LEU:HD12	2:D:571:GLU:HG2	1.98	0.46
2:E:545:SER:O	2:E:547:SER:N	2.49	0.46
1:A:108:THR:HG23	1:A:234:ASN:O	2.15	0.46
2:F:549:GLU:OE2	2:F:549:GLU:HA	2.15	0.46
1:B:130:VAL:HG22	1:B:168:PHE:H	1.81	0.46
2:F:355:ASP:OD2	2:F:357:ARG:NH1	2.44	0.46
1:A:559:PHE:CZ	1:C:43:PHE:CD2	3.04	0.46
1:B:84:LEU:O	1:B:237:ARG:CG	2.64	0.45
1:B:332:ILE:O	1:B:332:ILE:HG13	2.15	0.45
1:C:347:PHE:CE2	1:C:509:ARG:HG2	2.51	0.45
1:B:336:CYS:SG	1:B:358:ILE:HG23	2.57	0.45
1:C:417:LYS:HG2	1:C:453:TYR:OH	2.16	0.45
2:F:37:GLU:HB3	2:F:353:LYS:HG2	1.98	0.45
1:A:85:PRO:HD2	1:A:269:TYR:OH	2.17	0.45
1:A:877:LEU:HD13	1:A:1029:MET:SD	2.56	0.45
2:E:48:TRP:CZ3	2:E:357:ARG:HD2	2.51	0.45
1:B:642:VAL:CG1	1:B:649:CYS:SG	3.05	0.45
2:D:381:TYR:CD2	2:D:404:VAL:HG11	2.52	0.45
2:E:545:SER:C	2:E:547:SER:H	2.19	0.45
1:C:1082:CYS:HB2	1:C:1134:ASN:OD1	2.16	0.45
2:E:48:TRP:CE3	2:E:357:ARG:HD2	2.51	0.45
1:A:900:MET:HE2	1:B:1094:VAL:CG2	2.44	0.45
1:A:904:TYR:CZ	1:B:1107:ARG:HD3	2.51	0.45
2:D:212:VAL:HG23	2:D:215:TYR:HB2	1.97	0.45
1:A:616:ASN:ND2	4:A:1308:NAG:C2	2.70	0.44
1:C:500:THR:OG1	2:E:41:TYR:OH	2.27	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:642:VAL:HG13	1:B:649:CYS:SG	2.57	0.44
1:B:357:ARG:HD3	1:B:396:TYR:HE1	1.81	0.44
2:D:568:LEU:HD12	2:D:571:GLU:CG	2.47	0.44
1:A:1094:VAL:CG2	1:C:900:MET:CE	2.92	0.44
1:C:123:ALA:HB3	4:C:1302:NAG:H81	1.99	0.44
1:C:474:GLN:HA	1:C:488:CYS:HB3	2.00	0.44
2:F:478:TRP:O	2:F:482:ARG:HG3	2.18	0.44
1:A:411:ALA:HB1	1:A:412:PRO:CD	2.47	0.43
2:E:145:GLU:N	2:E:146:PRO:HD2	2.32	0.43
2:E:582:ARG:HD2	2:E:582:ARG:HA	1.40	0.43
2:E:177:ARG:HD3	2:E:497:TYR:O	2.18	0.43
1:A:123:ALA:C	1:A:125:ASN:N	2.70	0.43
1:A:461:LEU:CD2	1:A:462:LYS:H	2.30	0.43
1:B:904:TYR:OH	1:C:1094:VAL:HB	2.19	0.43
1:C:577:ARG:HB2	1:C:584:ILE:CD1	2.49	0.43
2:F:88:ILE:HG21	2:F:93:VAL:HG13	2.01	0.43
2:E:538:PRO:CB	2:E:540:HIS:HE1	2.32	0.43
1:A:717:ASN:ND2	4:A:1311:NAG:C7	2.80	0.43
1:C:1037:SER:H	1:C:1048:HIS:CD2	2.35	0.43
2:D:177:ARG:HB3	2:D:178:PRO:HD3	2.01	0.43
1:A:62:VAL:HG12	1:A:62:VAL:O	2.19	0.43
1:A:368:LEU:HD23	4:A:1306:NAG:C8	2.45	0.43
2:F:330:ASN:HB3	2:F:357:ARG:CZ	2.48	0.43
1:A:454:ARG:HG2	1:A:492:LEU:CD2	2.49	0.43
1:A:559:PHE:CD1	1:A:559:PHE:N	2.86	0.42
2:E:155:SER:O	2:E:161:ARG:HD2	2.19	0.42
1:A:339:GLY:HA2	1:A:343:ASN:HB2	2.00	0.42
2:E:177:ARG:HB3	2:E:178:PRO:CD	2.49	0.42
2:E:165:TRP:CH2	2:E:490:PRO:HD2	2.54	0.42
1:B:900:MET:HE1	1:C:1094:VAL:HG23	2.01	0.42
1:A:1136:THR:O	1:A:1136:THR:HG22	2.19	0.42
1:B:877:LEU:HD13	1:B:1029:MET:SD	2.59	0.42
1:A:351:TYR:HB2	1:A:454:ARG:HG3	2.01	0.42
2:E:192:ARG:HH21	2:E:192:ARG:CG	2.32	0.42
2:F:403:ALA:CB	2:F:518:ARG:HG2	2.43	0.42
2:E:177:ARG:HA	2:E:177:ARG:HD2	1.77	0.42
1:A:1100:THR:OG1	3:H:1:NAG:C8	2.68	0.41
1:C:1134:ASN:ND2	3:O:1:NAG:N2	2.68	0.41
2:D:514:ARG:O	2:D:518:ARG:HB2	2.20	0.41
1:A:742:ILE:HG12	1:A:1000:ARG:HB3	2.01	0.41
1:B:578:ASP:O	1:B:582:LEU:HD23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R:2:NAG:H83	3:R:2:NAG:H3	2.02	0.41
1:A:28:TYR:CE1	4:A:1301:NAG:C8	3.03	0.41
1:C:474:GLN:H	1:C:488:CYS:HB3	1.86	0.41
1:A:1100:THR:HB	3:H:1:NAG:HN2	1.85	0.41
1:B:96:GLU:OE1	1:B:190:ARG:NH1	2.46	0.41
2:E:54:ILE:HD11	2:E:343:VAL:HG13	2.02	0.41
1:C:31:SER:HB3	1:C:62:VAL:CG1	2.50	0.41
1:C:121:ASN:OD1	1:C:125:ASN:O	2.38	0.41
1:A:130:VAL:HB	1:A:233:ILE:CD1	2.51	0.41
1:A:472:ILE:CG2	1:A:488:CYS:SG	3.08	0.41
1:B:357:ARG:HG2	1:B:396:TYR:HD1	1.85	0.40
1:A:452:LEU:HD22	1:A:492:LEU:HB3	2.04	0.40
2:D:201:ASP:OD1	2:D:204:ARG:NE	2.39	0.40
2:F:330:ASN:O	2:F:357:ARG:HD3	2.19	0.40
2:D:165:TRP:CH2	2:D:490:PRO:HD2	2.56	0.40
2:F:54:ILE:HG13	2:F:341:LYS:HG3	2.04	0.40
2:F:88:ILE:HG12	2:F:88:ILE:H	1.73	0.40
1:A:351:TYR:CB	1:A:454:ARG:HG3	2.51	0.40
1:A:363:ALA:HB3	1:A:365:TYR:CE2	2.57	0.40
1:B:567:ARG:HG3	1:B:572:THR:O	2.22	0.40
1:C:132:GLU:OE1	4:C:1313:NAG:C7	2.70	0.40
1:C:336:CYS:HB2	1:C:363:ALA:HA	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	959/1234 (78%)	887 (92%)	68 (7%)	4 (0%)	30 60
1	B	959/1234 (78%)	894 (93%)	61 (6%)	4 (0%)	30 60
1	C	959/1234 (78%)	882 (92%)	73 (8%)	4 (0%)	30 60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	591/615 (96%)	565 (96%)	21 (4%)	5 (1%)	16	44
2	E	591/615 (96%)	560 (95%)	29 (5%)	2 (0%)	37	66
2	F	591/615 (96%)	555 (94%)	31 (5%)	5 (1%)	16	44
All	All	4650/5547 (84%)	4343 (93%)	283 (6%)	24 (0%)	27	54

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	569	ILE
1	C	417	LYS
2	D	106	SER
2	F	144	LEU
1	C	582	LEU
2	E	546	ASN
2	F	353	LYS
1	C	483	VAL
2	F	546	ASN
1	A	381	GLY
1	B	582	LEU
1	C	123	ALA
2	D	325	GLN
1	A	459	SER
2	D	104	GLY
2	F	52	THR
2	F	147	GLY
1	A	474	GLN
1	B	381	GLY
2	D	339	VAL
1	B	483	VAL
2	E	339	VAL
2	D	284	PRO
1	B	332	ILE

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	858/1069 (80%)	840 (98%)	18 (2%)	48	69
1	B	860/1069 (80%)	842 (98%)	18 (2%)	48	69
1	C	859/1069 (80%)	842 (98%)	17 (2%)	50	70
2	D	524/540 (97%)	512 (98%)	12 (2%)	45	67
2	E	524/540 (97%)	513 (98%)	11 (2%)	48	69
2	F	524/540 (97%)	505 (96%)	19 (4%)	30	56
All	All	4149/4827 (86%)	4054 (98%)	95 (2%)	46	67

All (95) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	ARG
1	A	266	TYR
1	A	336	CYS
1	A	353	TRP
1	A	403	ARG
1	A	414	GLN
1	A	422	ASN
1	A	429	PHE
1	A	437	ASN
1	A	453	TYR
1	A	460	ASN
1	A	461	LEU
1	A	466	ARG
1	A	488	CYS
1	A	489	TYR
1	A	711	SER
1	A	1032	CYS
1	A	1076	THR
1	B	120	VAL
1	B	122	ASN
1	B	124	THR
1	B	350	VAL
1	B	377	PHE
1	B	379	CYS
1	B	382	VAL
1	B	391	CYS
1	B	402	ILE
1	B	427	ASP
1	B	432	CYS
1	B	460	ASN

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Mol	Chain	Res	Type
1	B	523	THR
1	B	525	CYS
1	B	567	ARG
1	B	1032	CYS
1	B	1084	ASP
1	B	1107	ARG
1	C	88	ASP
1	C	132	GLU
1	C	237	ARG
1	C	336	CYS
1	C	357	ARG
1	C	369	TYR
1	C	480	CYS
1	C	488	CYS
1	C	538	CYS
1	C	546	LEU
1	C	581	THR
1	C	656	VAL
1	C	796	ASP
1	C	901	GLN
1	C	995	ARG
1	C	1084	ASP
1	C	1092	GLU
2	D	97	LEU
2	D	201	ASP
2	D	202	TYR
2	D	318	VAL
2	D	335	ASP
2	D	343	VAL
2	D	357	ARG
2	D	371	THR
2	D	401	HIS
2	D	411	SER
2	D	514	ARG
2	D	571	GLU
2	E	133	CYS
2	E	149	ASN
2	E	335	ASP
2	E	361	CYS
2	E	368	ASP
2	E	381	TYR
2	E	514	ARG

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Mol	Chain	Res	Type
2	E	518	ARG
2	E	571	GLU
2	E	578	ASN
2	E	582	ARG
2	F	54	ILE
2	F	55	THR
2	F	88	ILE
2	F	93	VAL
2	F	133	CYS
2	F	183	TYR
2	F	273	ARG
2	F	335	ASP
2	F	356	PHE
2	F	361	CYS
2	F	381	TYR
2	F	404	VAL
2	F	411	SER
2	F	449	THR
2	F	514	ARG
2	F	518	ARG
2	F	559	ARG
2	F	571	GLU
2	F	582	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	234	ASN
1	A	343	ASN
1	A	616	ASN
1	A	655	HIS
1	A	895	GLN
1	A	1074	ASN
1	A	1098	ASN
1	A	1101	HIS
1	A	1135	ASN
1	B	61	ASN
1	B	122	ASN
1	B	164	ASN
1	B	165	ASN
1	B	234	ASN
1	B	282	ASN

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Mol	Chain	Res	Type
1	B	603	ASN
1	B	1074	ASN
1	C	165	ASN
1	C	234	ASN
1	C	343	ASN
1	C	603	ASN
1	C	895	GLN
1	C	1048	HIS
1	C	1074	ASN
1	C	1134	ASN
2	E	58	ASN
2	E	417	HIS
2	F	63	ASN
2	F	81	GLN
2	F	89	GLN
2	F	103	ASN
2	F	134	ASN
2	F	322	ASN
2	F	432	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

48 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	NAG	G	1	3,1	14,14,15	1.25	2 (14%)	17,19,21	0.65	0
3	NAG	G	2	3	14,14,15	1.11	1 (7%)	17,19,21	0.99	2 (11%)
3	NAG	H	1	3	14,14,15	1.52	2 (14%)	17,19,21	0.78	0
3	NAG	H	2	3	14,14,15	1.40	2 (14%)	17,19,21	0.92	1 (5%)
3	NAG	I	1	3,1	14,14,15	1.53	2 (14%)	17,19,21	0.69	0
3	NAG	I	2	3	14,14,15	1.52	2 (14%)	17,19,21	0.63	0
3	NAG	J	1	3,1	14,14,15	1.21	2 (14%)	17,19,21	0.92	1 (5%)
3	NAG	J	2	3	14,14,15	1.20	1 (7%)	17,19,21	0.64	0
3	NAG	K	1	3,1	14,14,15	1.35	2 (14%)	17,19,21	0.82	1 (5%)
3	NAG	K	2	3	14,14,15	1.36	2 (14%)	17,19,21	0.72	0
3	NAG	L	1	3,1	14,14,15	1.51	2 (14%)	17,19,21	0.71	0
3	NAG	L	2	3	14,14,15	1.48	2 (14%)	17,19,21	0.73	0
3	NAG	M	1	3,1	14,14,15	1.18	2 (14%)	17,19,21	0.79	0
3	NAG	M	2	3	14,14,15	1.13	1 (7%)	17,19,21	0.76	0
3	NAG	N	1	3,1	14,14,15	1.33	3 (21%)	17,19,21	0.96	0
3	NAG	N	2	3	14,14,15	1.37	2 (14%)	17,19,21	0.90	1 (5%)
3	NAG	O	1	3	14,14,15	1.52	2 (14%)	17,19,21	0.70	0
3	NAG	O	2	3	14,14,15	1.35	2 (14%)	17,19,21	1.02	2 (11%)
3	NAG	P	1	2,3	14,14,15	0.29	0	17,19,21	0.55	0
3	NAG	P	2	3	14,14,15	0.29	0	17,19,21	0.53	0
3	NAG	Q	1	2,3	14,14,15	0.39	0	17,19,21	0.66	0
3	NAG	Q	2	3	14,14,15	0.99	1 (7%)	17,19,21	1.00	1 (5%)
3	NAG	R	1	2,3	14,14,15	0.29	0	17,19,21	0.58	0
3	NAG	R	2	3	14,14,15	0.30	0	17,19,21	0.56	0
3	NAG	S	1	2,3	14,14,15	0.31	0	17,19,21	0.53	0
3	NAG	S	2	3	14,14,15	1.19	1 (7%)	17,19,21	0.89	0
3	NAG	T	1	3	14,14,15	0.24	0	17,19,21	0.63	0
3	NAG	T	2	3	14,14,15	0.37	0	17,19,21	0.61	1 (5%)
3	NAG	U	1	2,3	14,14,15	0.58	0	17,19,21	0.74	0
3	NAG	U	2	3	14,14,15	0.57	0	17,19,21	0.38	0
3	NAG	V	1	2,3	14,14,15	0.40	0	17,19,21	0.66	0
3	NAG	V	2	3	14,14,15	0.27	0	17,19,21	0.70	1 (5%)
3	NAG	W	1	2,3	14,14,15	1.45	4 (28%)	17,19,21	1.38	2 (11%)
3	NAG	W	2	3	14,14,15	1.17	1 (7%)	17,19,21	0.88	0
3	NAG	X	1	2,3	14,14,15	1.51	4 (28%)	17,19,21	1.10	2 (11%)
3	NAG	X	2	3	14,14,15	1.28	1 (7%)	17,19,21	0.79	0
3	NAG	Y	1	2,3	14,14,15	0.23	0	17,19,21	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	NAG	Y	2	3	14,14,15	0.39	0	17,19,21	0.61	1 (5%)
3	NAG	Z	1	2,3	14,14,15	0.58	1 (7%)	17,19,21	0.74	0
3	NAG	Z	2	3	14,14,15	0.55	0	17,19,21	0.38	0
3	NAG	a	1	2,3	14,14,15	0.42	0	17,19,21	0.67	0
3	NAG	a	2	3	14,14,15	0.29	0	17,19,21	0.71	1 (5%)
3	NAG	b	1	3	14,14,15	0.19	0	17,19,21	0.71	1 (5%)
3	NAG	b	2	3	14,14,15	1.30	2 (14%)	17,19,21	2.08	4 (23%)
3	NAG	c	1	3	14,14,15	0.39	0	17,19,21	0.52	0
3	NAG	c	2	3	14,14,15	1.11	1 (7%)	17,19,21	1.23	1 (5%)
3	NAG	d	1	2,3	14,14,15	0.23	0	17,19,21	0.63	0
3	NAG	d	2	3	14,14,15	0.39	0	17,19,21	0.61	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	G	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	NAG	H	1	3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	NAG	I	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	0/6/23/26	0/1/1/1
3	NAG	J	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1
3	NAG	K	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	K	2	3	-	1/6/23/26	0/1/1/1
3	NAG	L	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
3	NAG	M	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	0/6/23/26	0/1/1/1
3	NAG	N	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	N	2	3	-	0/6/23/26	0/1/1/1
3	NAG	O	1	3	-	1/6/23/26	0/1/1/1
3	NAG	O	2	3	-	0/6/23/26	0/1/1/1
3	NAG	P	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	P	2	3	-	2/6/23/26	0/1/1/1
3	NAG	Q	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	R	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	R	2	3	-	3/6/23/26	0/1/1/1
3	NAG	S	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	S	2	3	-	0/6/23/26	0/1/1/1
3	NAG	T	1	3	-	0/6/23/26	0/1/1/1
3	NAG	T	2	3	-	2/6/23/26	0/1/1/1
3	NAG	U	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	U	2	3	-	2/6/23/26	0/1/1/1
3	NAG	V	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	V	2	3	-	2/6/23/26	0/1/1/1
3	NAG	W	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	W	2	3	-	0/6/23/26	0/1/1/1
3	NAG	X	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	X	2	3	-	0/6/23/26	0/1/1/1
3	NAG	Y	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	Y	2	3	-	2/6/23/26	0/1/1/1
3	NAG	Z	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	Z	2	3	-	2/6/23/26	0/1/1/1
3	NAG	a	1	2,3	-	2/6/23/26	0/1/1/1
3	NAG	a	2	3	-	2/6/23/26	0/1/1/1
3	NAG	b	1	3	-	2/6/23/26	0/1/1/1
3	NAG	b	2	3	-	4/6/23/26	0/1/1/1
3	NAG	c	1	3	-	0/6/23/26	0/1/1/1
3	NAG	c	2	3	-	2/6/23/26	0/1/1/1
3	NAG	d	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	d	2	3	-	2/6/23/26	0/1/1/1

All (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	1	NAG	C1-C2	4.11	1.57	1.52
3	I	2	NAG	C1-C2	4.06	1.57	1.52
3	O	1	NAG	C1-C2	4.03	1.57	1.52
3	L	1	NAG	C1-C2	4.03	1.57	1.52
3	I	1	NAG	C1-C2	4.01	1.57	1.52
3	H	2	NAG	C1-C2	3.69	1.57	1.52
3	O	2	NAG	C1-C2	3.65	1.57	1.52
3	L	2	NAG	C1-C2	3.58	1.57	1.52
3	S	2	NAG	O5-C5	3.34	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	b	2	NAG	O5-C5	3.29	1.49	1.43
3	N	2	NAG	O5-C5	3.23	1.49	1.43
3	X	1	NAG	O5-C5	3.20	1.49	1.43
3	W	1	NAG	O5-C5	3.16	1.49	1.43
3	L	2	NAG	O5-C5	3.05	1.49	1.43
3	c	2	NAG	O5-C5	3.03	1.49	1.43
3	N	1	NAG	O5-C5	3.02	1.49	1.43
3	G	1	NAG	O5-C5	2.71	1.48	1.43
3	K	1	NAG	O4-C4	2.70	1.49	1.43
3	J	1	NAG	O5-C5	2.63	1.48	1.43
3	K	2	NAG	C1-C2	2.61	1.55	1.52
3	K	1	NAG	O5-C5	2.59	1.48	1.43
3	N	2	NAG	O5-C1	2.55	1.48	1.43
3	X	2	NAG	O5-C5	2.52	1.48	1.43
3	M	2	NAG	O5-C5	2.51	1.48	1.43
3	X	1	NAG	O5-C1	2.47	1.47	1.43
3	K	2	NAG	O5-C5	2.47	1.48	1.43
3	J	2	NAG	O5-C5	2.43	1.48	1.43
3	H	1	NAG	O5-C5	2.42	1.48	1.43
3	I	2	NAG	O5-C5	2.42	1.48	1.43
3	H	2	NAG	O5-C5	2.39	1.48	1.43
3	X	1	NAG	C1-C2	2.37	1.55	1.52
3	W	2	NAG	O5-C5	2.36	1.48	1.43
3	Q	2	NAG	O5-C5	2.36	1.48	1.43
3	O	1	NAG	O5-C5	2.35	1.48	1.43
3	b	2	NAG	C8-C7	2.33	1.55	1.50
3	L	1	NAG	O5-C5	2.32	1.48	1.43
3	I	1	NAG	O5-C5	2.29	1.47	1.43
3	X	1	NAG	O4-C4	2.28	1.48	1.43
3	W	1	NAG	O4-C4	2.25	1.48	1.43
3	N	1	NAG	O4-C4	2.20	1.48	1.43
3	M	1	NAG	O5-C5	2.20	1.47	1.43
3	O	2	NAG	O5-C5	2.19	1.47	1.43
3	J	1	NAG	O4-C4	2.19	1.48	1.43
3	G	2	NAG	O5-C5	2.16	1.47	1.43
3	W	1	NAG	O5-C1	2.13	1.47	1.43
3	M	1	NAG	C1-C2	2.12	1.55	1.52
3	G	1	NAG	O4-C4	2.06	1.48	1.43
3	W	1	NAG	C1-C2	2.03	1.55	1.52
3	N	1	NAG	C1-C2	2.03	1.55	1.52
3	Z	1	NAG	O5-C1	-2.01	1.40	1.43

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	b	2	NAG	C2-N2-C7	5.69	130.52	122.90
3	c	2	NAG	C1-O5-C5	4.33	117.99	112.19
3	b	2	NAG	C8-C7-N2	4.08	122.88	116.12
3	Q	2	NAG	C1-O5-C5	3.72	117.17	112.19
3	W	1	NAG	C1-O5-C5	3.59	117.00	112.19
3	W	1	NAG	C4-C3-C2	-3.01	106.60	111.02
3	X	1	NAG	C4-C3-C2	-2.85	106.84	111.02
3	b	2	NAG	O7-C7-N2	-2.77	117.08	121.98
3	b	2	NAG	C1-O5-C5	2.77	115.90	112.19
3	X	1	NAG	C1-O5-C5	2.75	115.88	112.19
3	H	2	NAG	C1-O5-C5	2.71	115.82	112.19
3	a	2	NAG	C1-O5-C5	2.49	115.52	112.19
3	V	2	NAG	C1-O5-C5	2.47	115.49	112.19
3	G	2	NAG	C1-O5-C5	2.43	115.44	112.19
3	G	2	NAG	O5-C1-C2	-2.36	107.64	111.29
3	K	1	NAG	C1-O5-C5	2.30	115.27	112.19
3	N	2	NAG	C1-O5-C5	2.25	115.20	112.19
3	J	1	NAG	C4-C3-C2	-2.21	107.77	111.02
3	b	1	NAG	C1-O5-C5	2.17	115.09	112.19
3	T	2	NAG	C1-O5-C5	2.09	114.98	112.19
3	Y	2	NAG	C1-O5-C5	2.07	114.96	112.19
3	d	2	NAG	C1-O5-C5	2.06	114.95	112.19
3	O	2	NAG	C4-C3-C2	2.04	114.00	111.02
3	O	2	NAG	C1-O5-C5	2.03	114.90	112.19

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	R	1	NAG	O7-C7-N2-C2
3	R	2	NAG	C3-C2-N2-C7
3	R	2	NAG	C8-C7-N2-C2
3	R	2	NAG	O7-C7-N2-C2
3	R	1	NAG	C8-C7-N2-C2
3	T	2	NAG	O5-C5-C6-O6
3	Y	2	NAG	O5-C5-C6-O6
3	d	2	NAG	O5-C5-C6-O6
3	b	2	NAG	C8-C7-N2-C2
3	U	1	NAG	O5-C5-C6-O6
3	Z	1	NAG	O5-C5-C6-O6
3	V	2	NAG	O5-C5-C6-O6
3	a	2	NAG	O5-C5-C6-O6
3	Q	1	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	V	1	NAG	O5-C5-C6-O6
3	a	1	NAG	O5-C5-C6-O6
3	b	1	NAG	O5-C5-C6-O6
3	V	2	NAG	C4-C5-C6-O6
3	a	2	NAG	C4-C5-C6-O6
3	b	1	NAG	C4-C5-C6-O6
3	U	2	NAG	C4-C5-C6-O6
3	Z	2	NAG	C4-C5-C6-O6
3	b	2	NAG	O7-C7-N2-C2
3	T	2	NAG	C4-C5-C6-O6
3	Y	2	NAG	C4-C5-C6-O6
3	d	2	NAG	C4-C5-C6-O6
3	U	1	NAG	C4-C5-C6-O6
3	Z	1	NAG	C4-C5-C6-O6
3	U	2	NAG	O5-C5-C6-O6
3	Z	2	NAG	O5-C5-C6-O6
3	Q	1	NAG	C4-C5-C6-O6
3	V	1	NAG	C4-C5-C6-O6
3	a	1	NAG	C4-C5-C6-O6
3	P	2	NAG	C4-C5-C6-O6
3	c	2	NAG	O5-C5-C6-O6
3	P	2	NAG	O5-C5-C6-O6
3	P	1	NAG	C4-C5-C6-O6
3	b	2	NAG	C3-C2-N2-C7
3	P	1	NAG	O5-C5-C6-O6
3	K	2	NAG	C1-C2-N2-C7
3	L	1	NAG	C1-C2-N2-C7
3	O	1	NAG	C1-C2-N2-C7
3	b	2	NAG	C1-C2-N2-C7
3	c	2	NAG	C1-C2-N2-C7

There are no ring outliers.

8 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	R	1	NAG	3	0
3	V	1	NAG	3	0
3	H	1	NAG	6	0
3	Z	1	NAG	2	0
3	O	1	NAG	4	0
3	U	1	NAG	2	0
3	T	1	NAG	3	0

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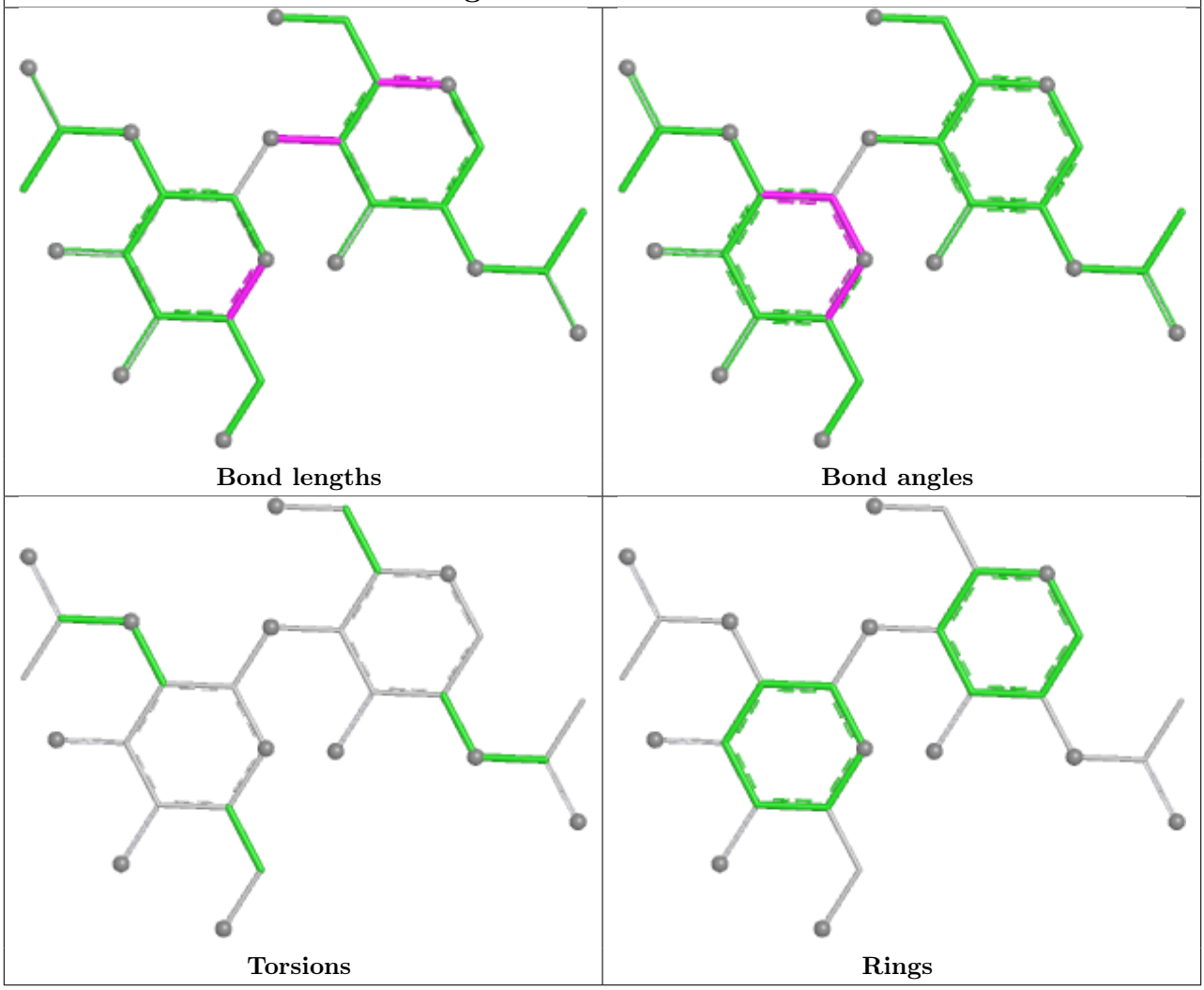
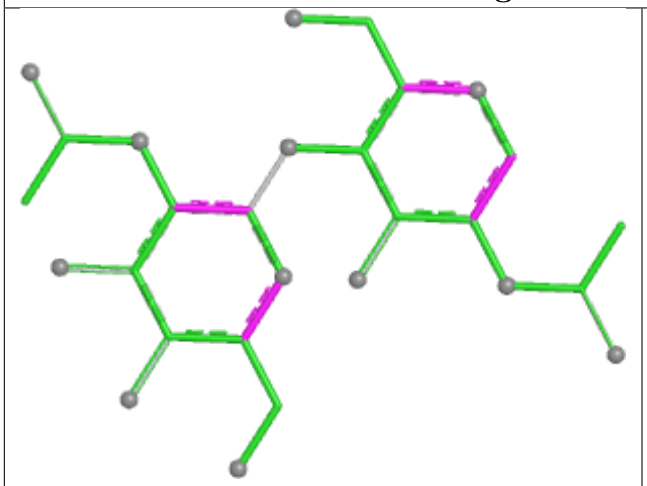
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	R	2	NAG	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

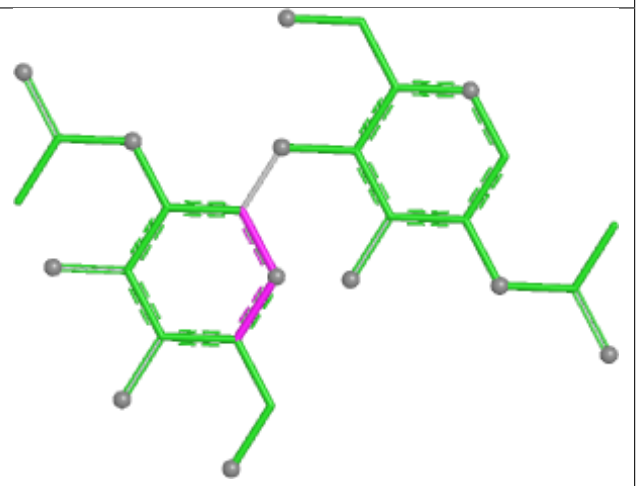
Oligosaccharide Chain G



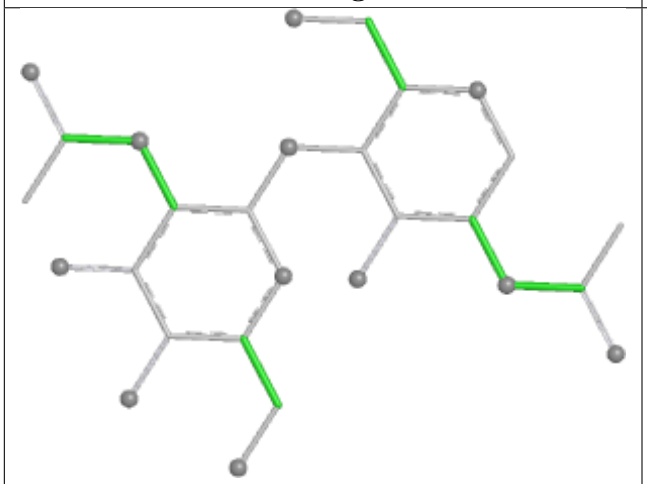
Oligosaccharide Chain H



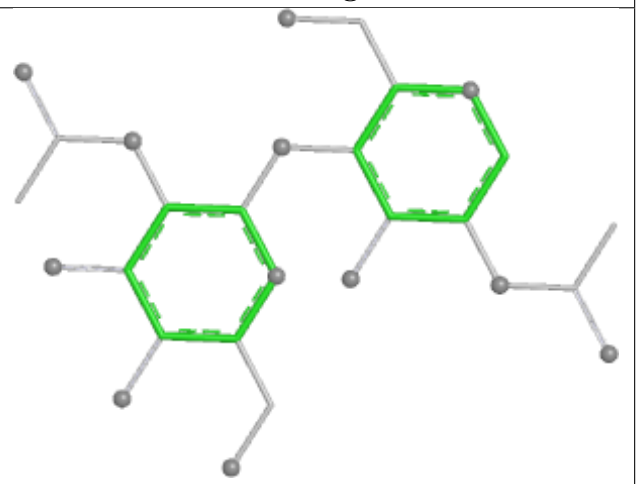
Bond lengths



Bond angles

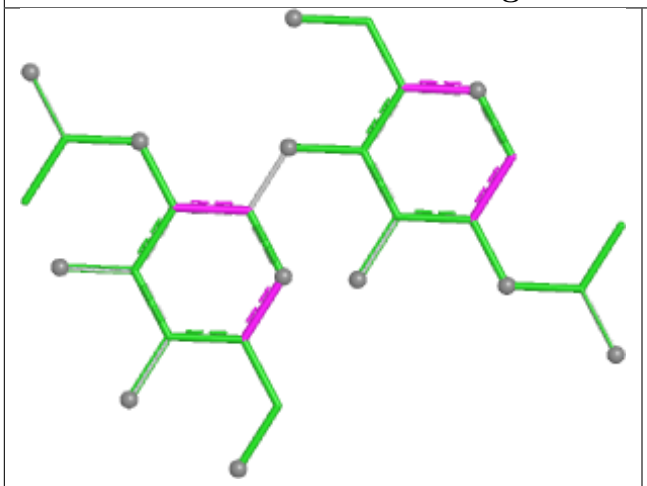


Torsions

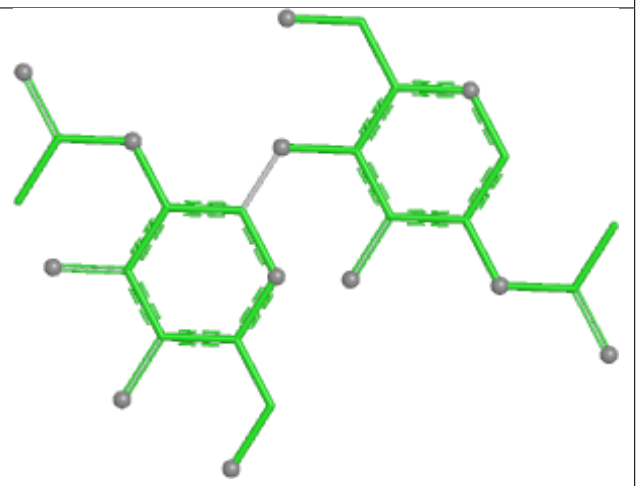


Rings

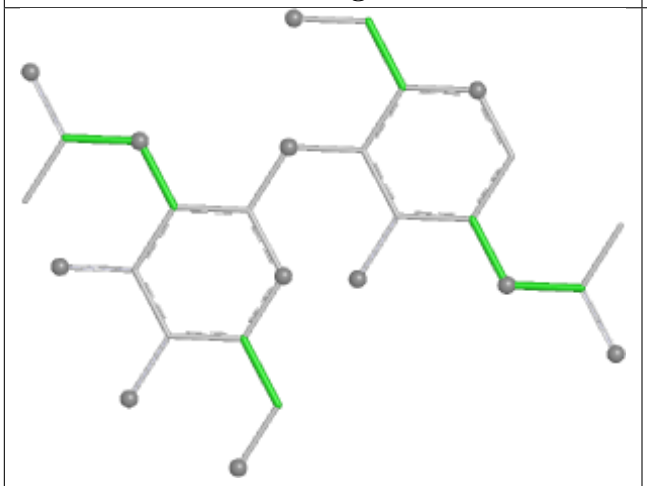
Oligosaccharide Chain I



Bond lengths



Bond angles



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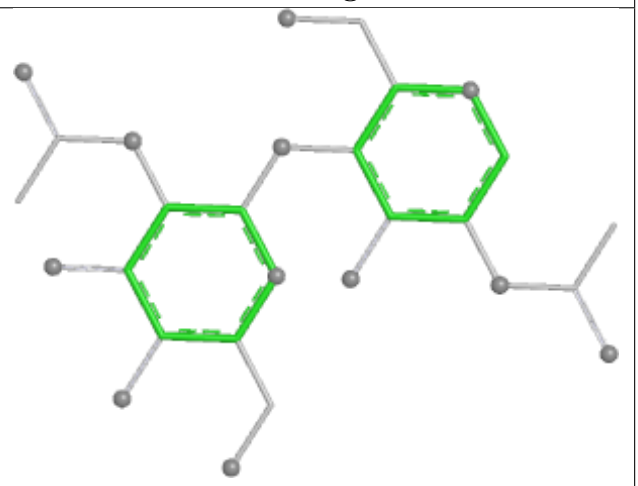
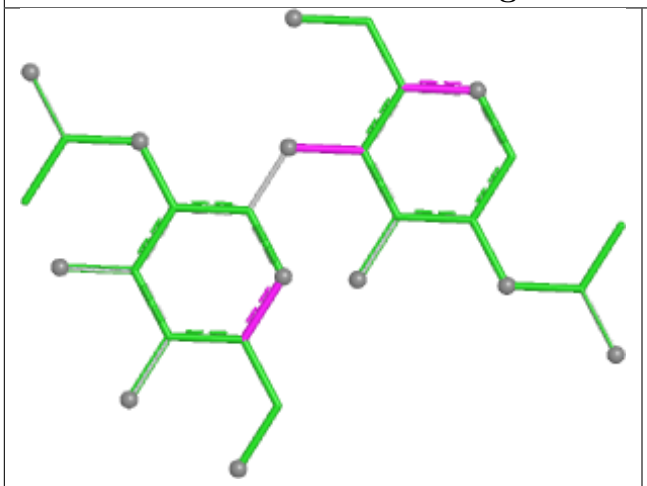
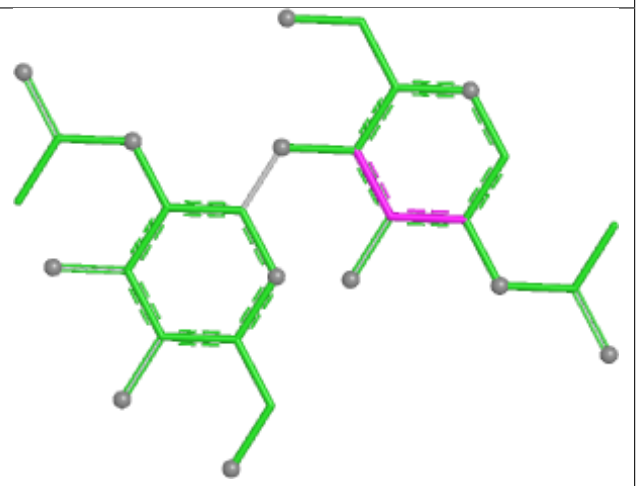


Rings

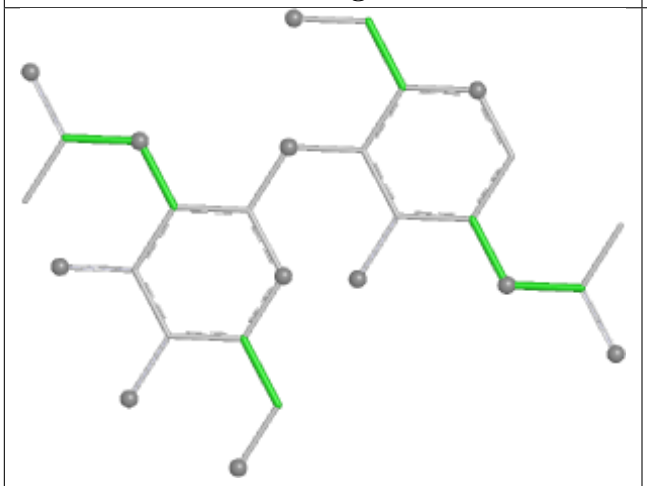
Oligosaccharide Chain J



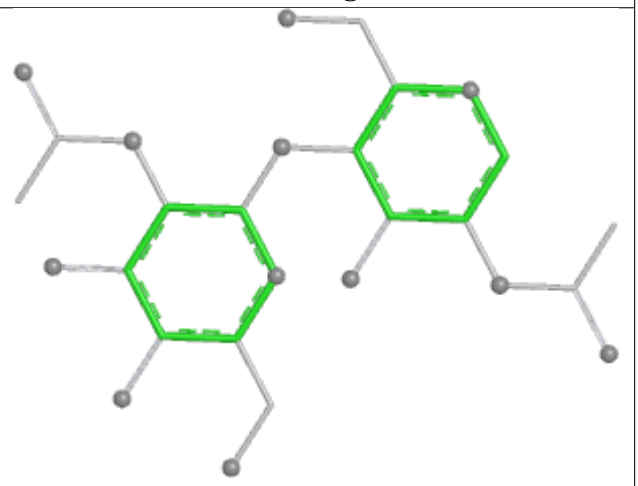
Bond lengths



Bond angles

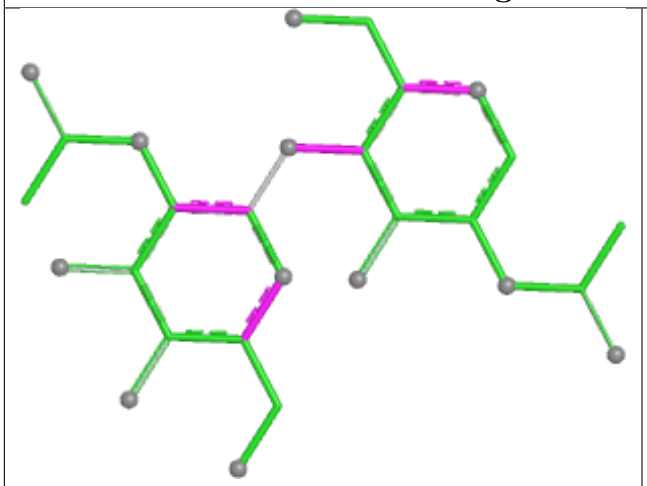


Torsions

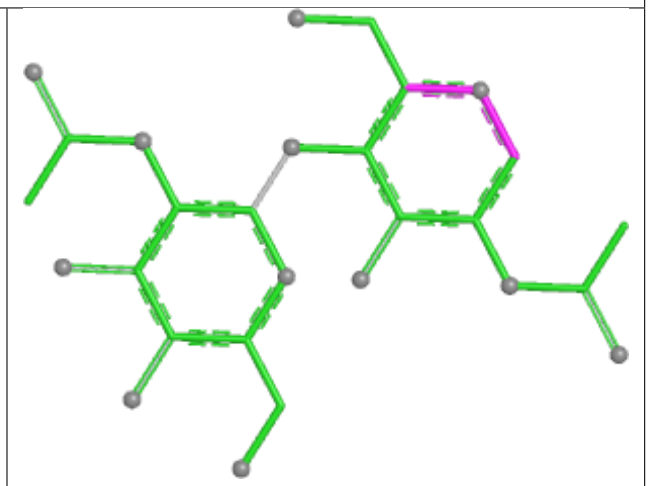


Rings

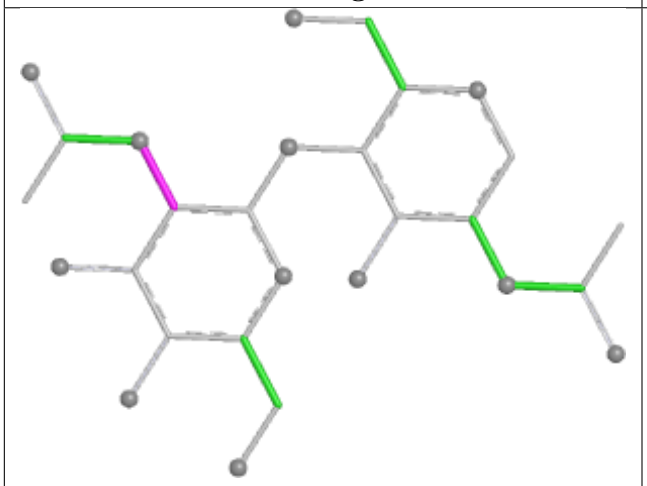
Oligosaccharide Chain K



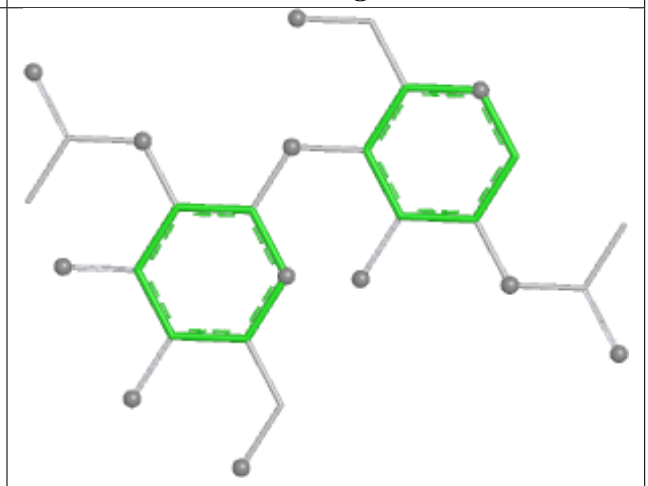
Bond lengths



Bond angles

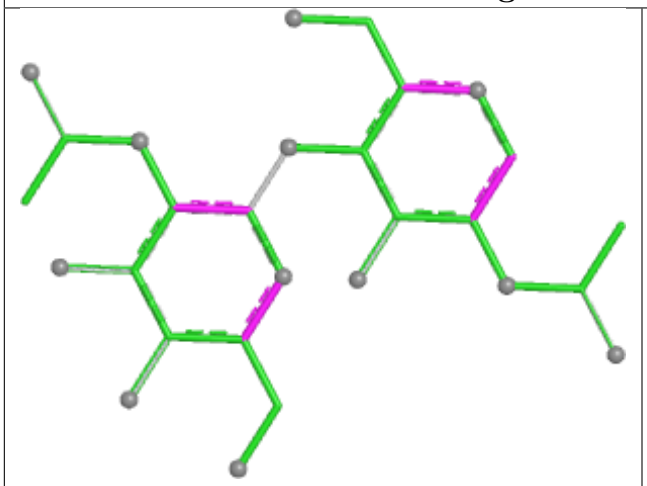


Torsions

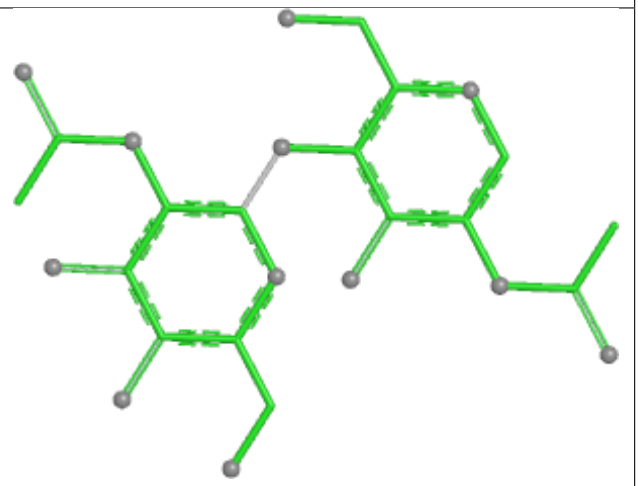


Rings

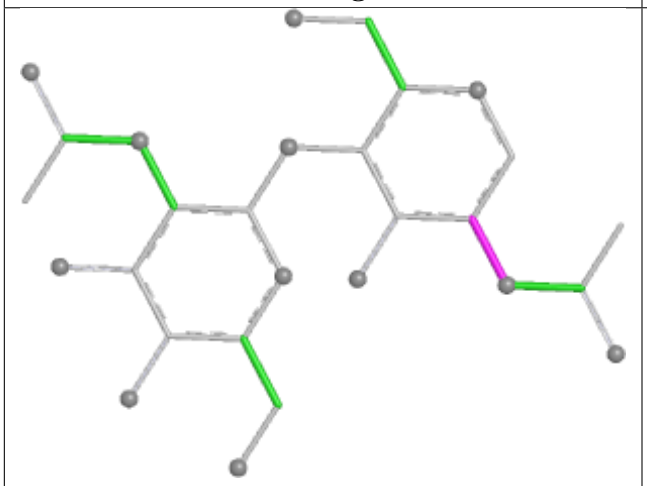
Oligosaccharide Chain L



Bond lengths



Bond angles



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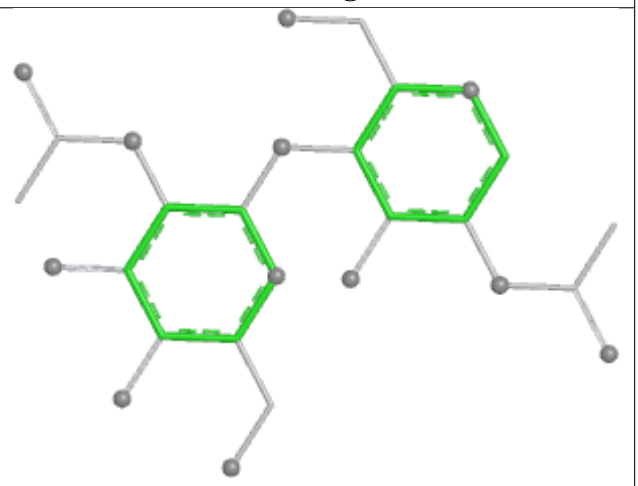
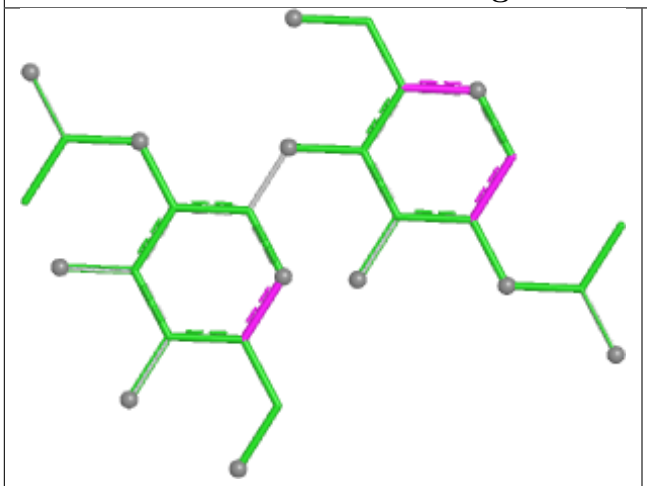


Rings

Oligosaccharide Chain M



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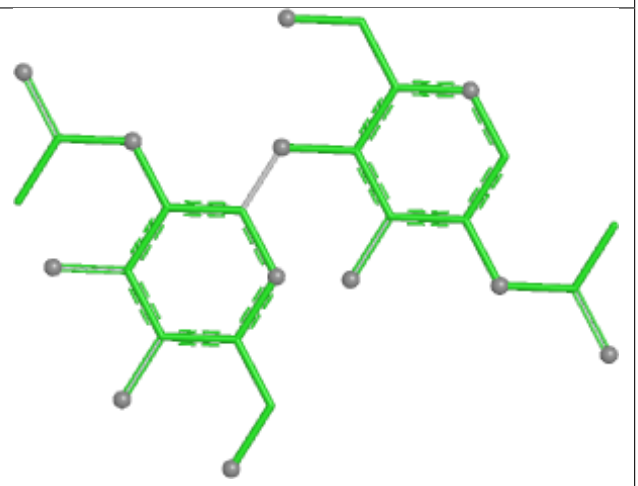
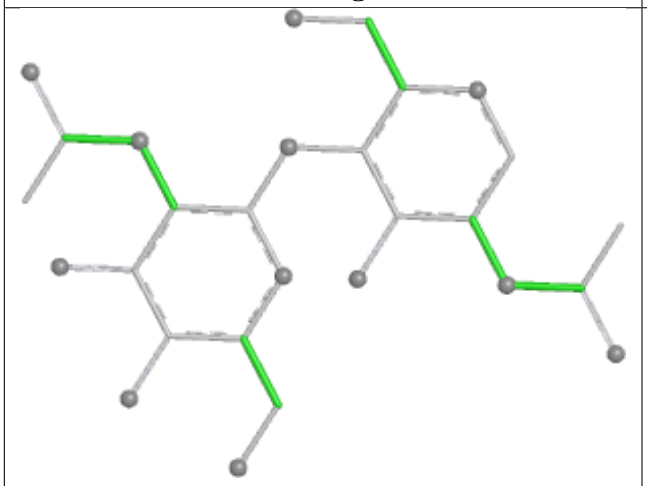


Bond angles



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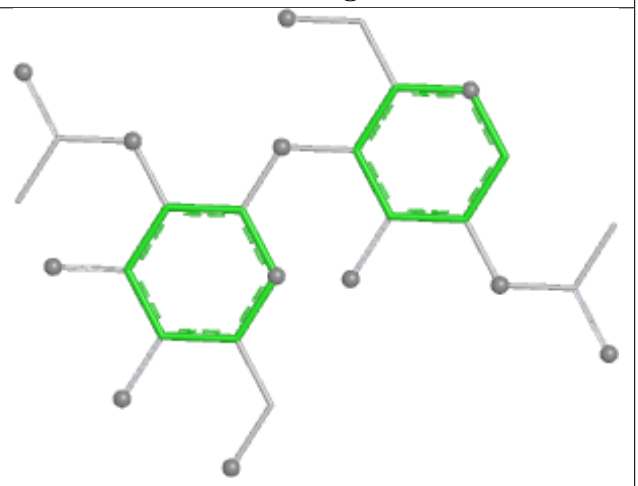
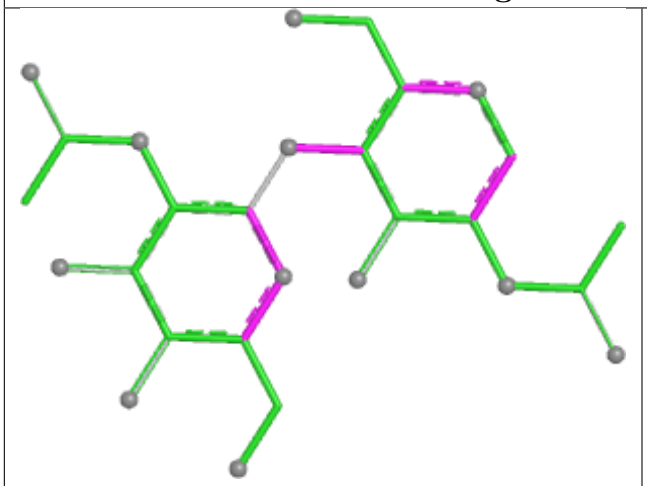
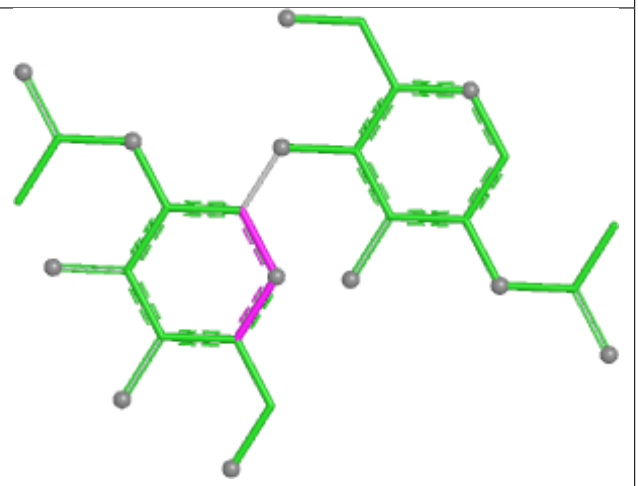


Rings

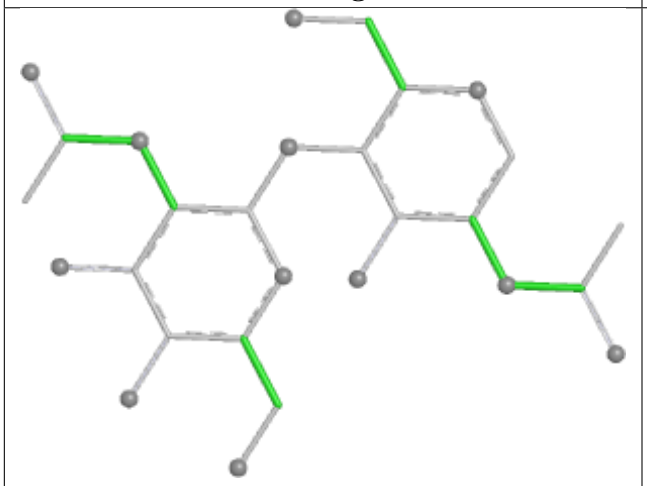
Oligosaccharide Chain N



Bond lengths



Bond angles



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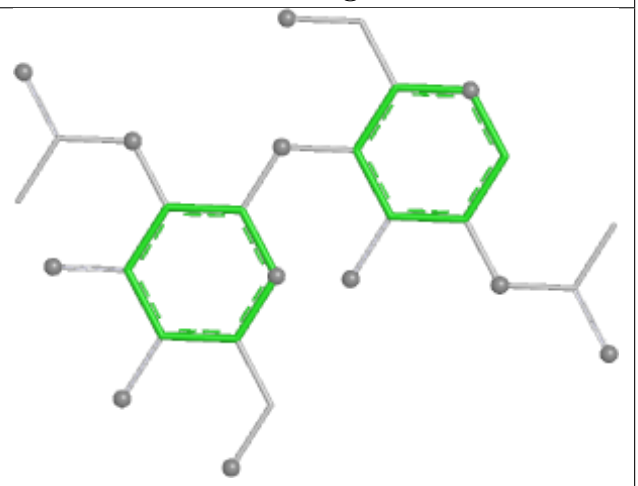
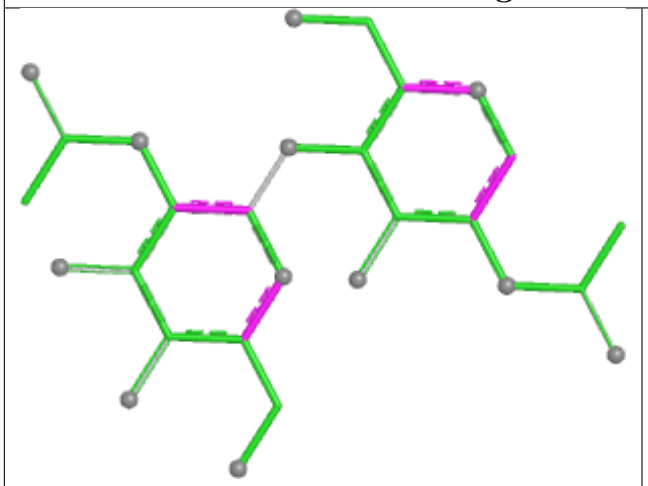


Rings

Oligosaccharide Chain O



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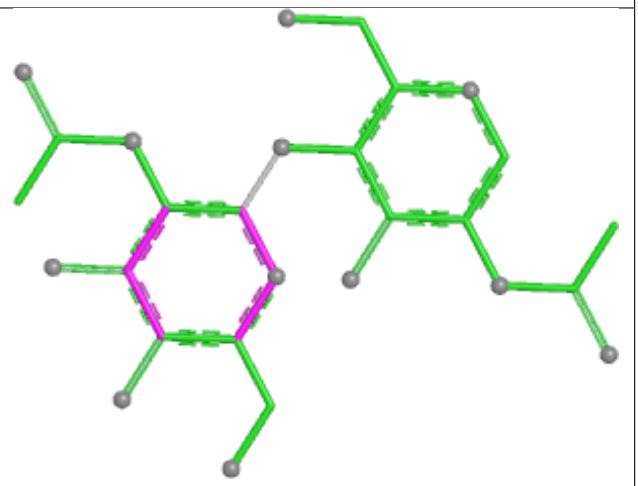
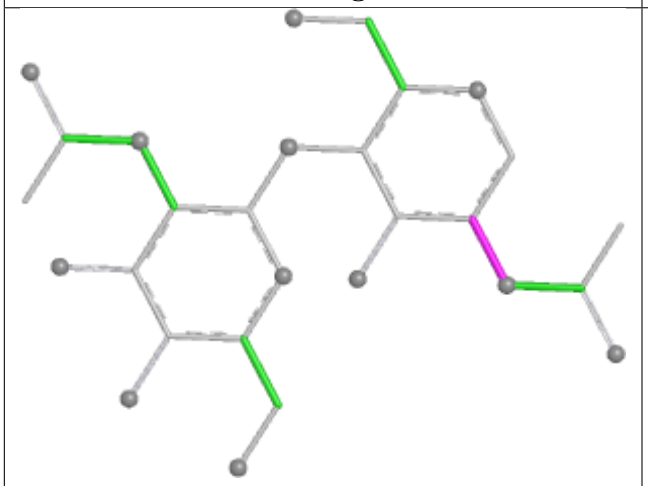


Bond angles



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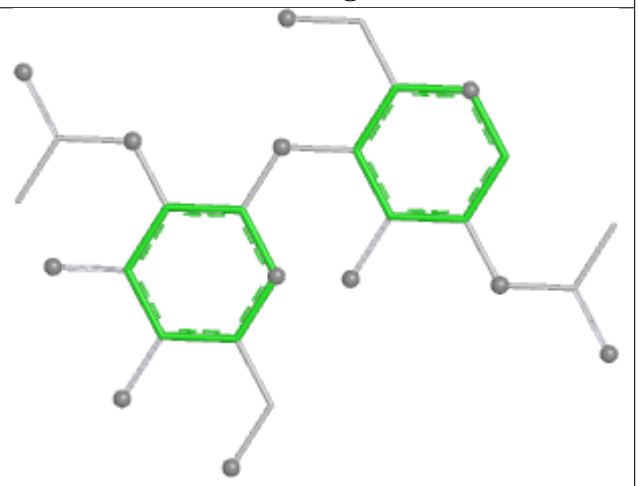
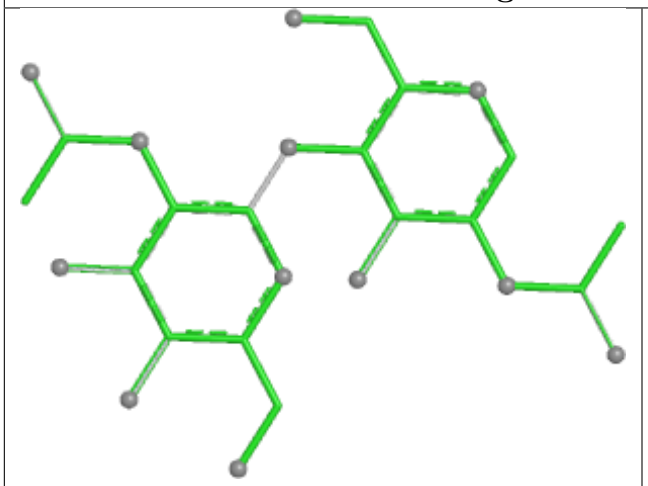
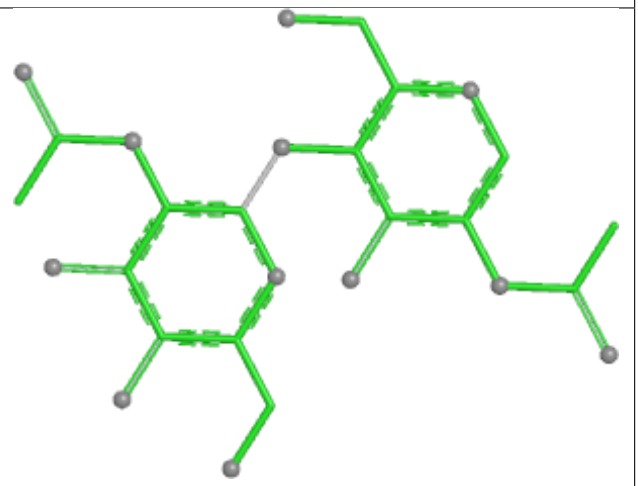


Rings

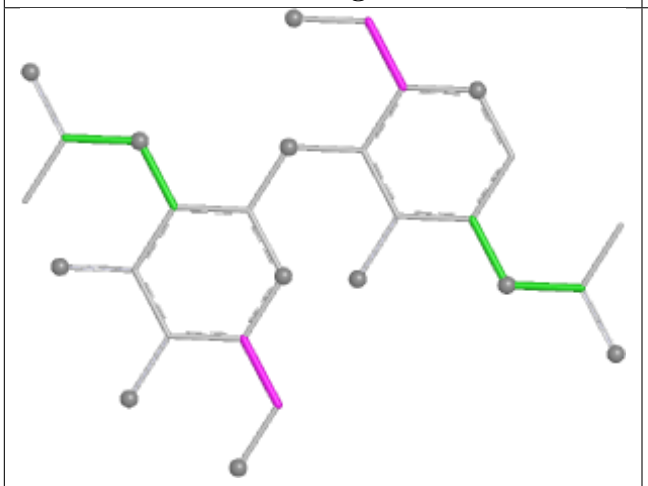
Oligosaccharide Chain P



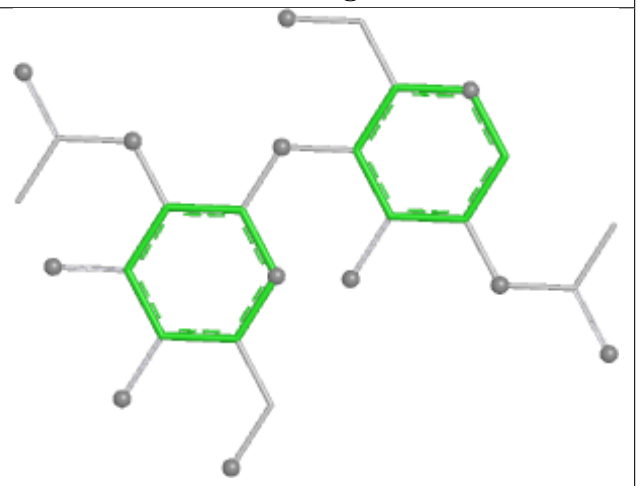
Bond lengths



Bond angles

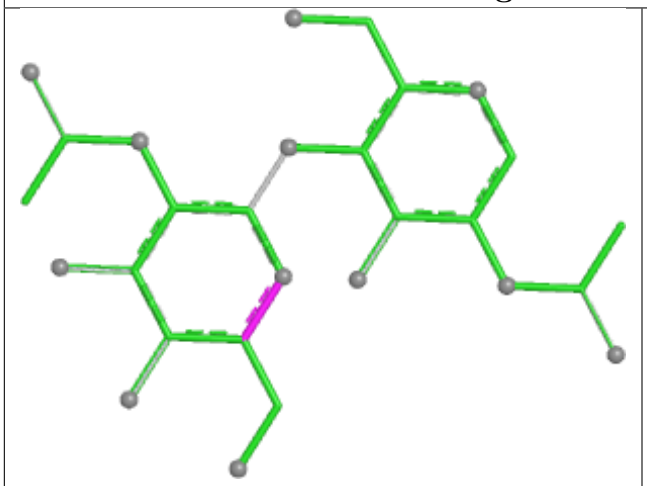


Torsions



Rings

Oligosaccharide Chain Q



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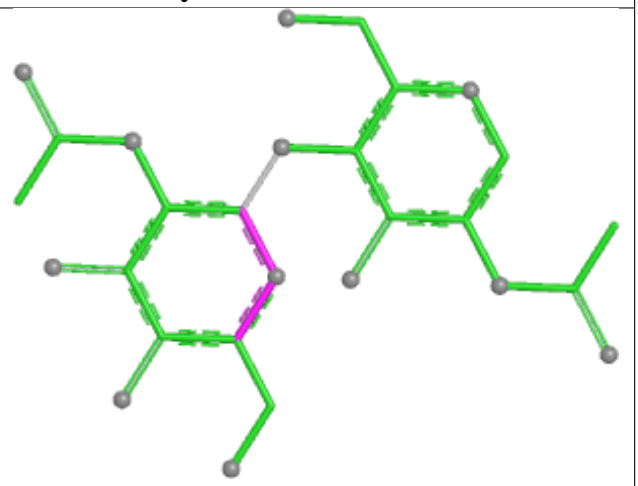
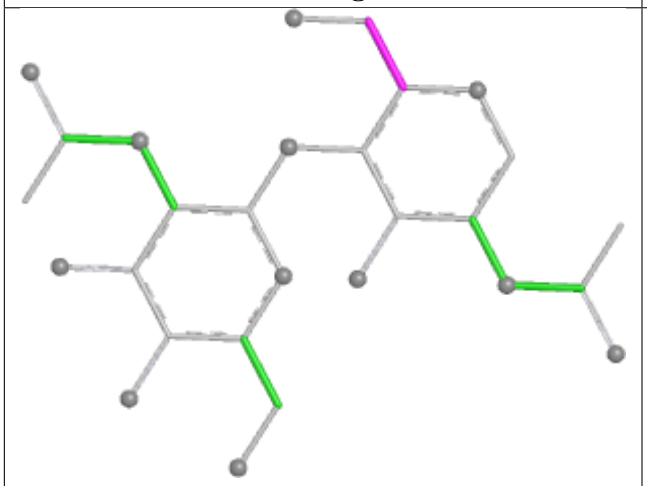
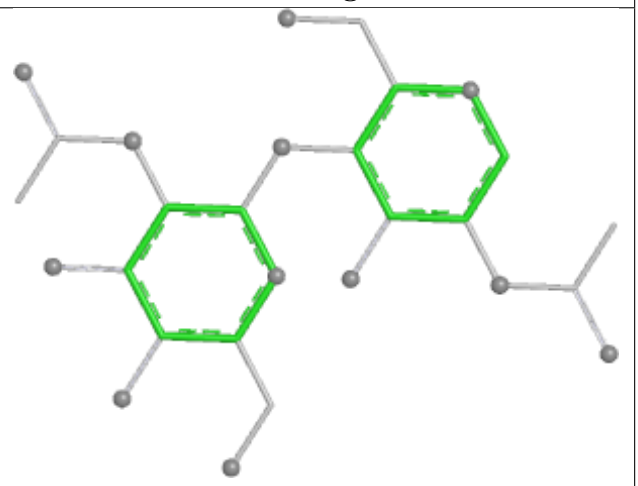


Bond angles

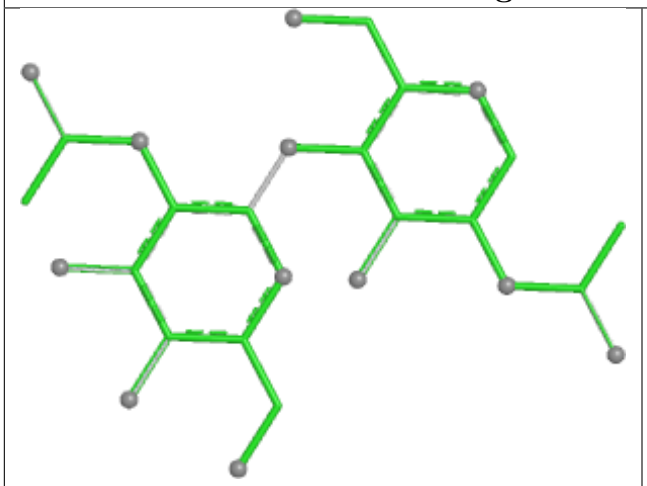


Torsions



Rings

Oligosaccharide Chain R



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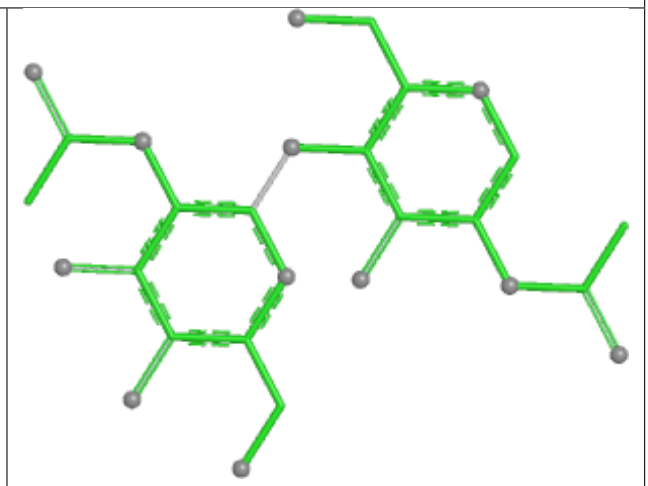

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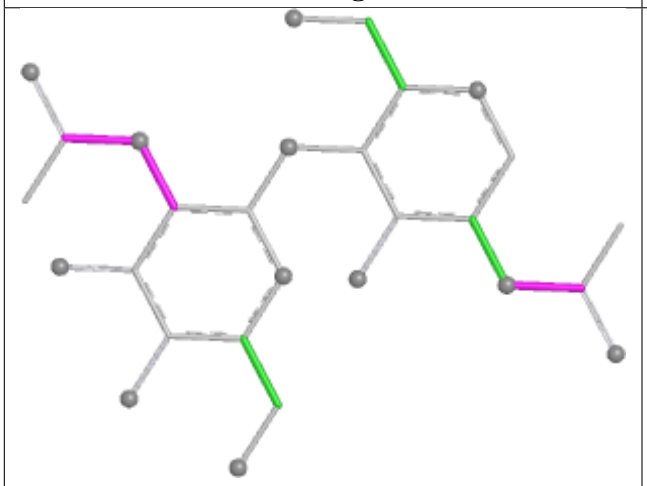

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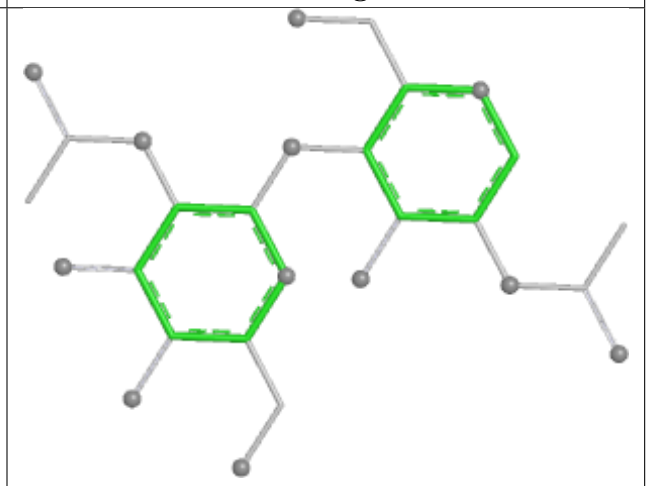
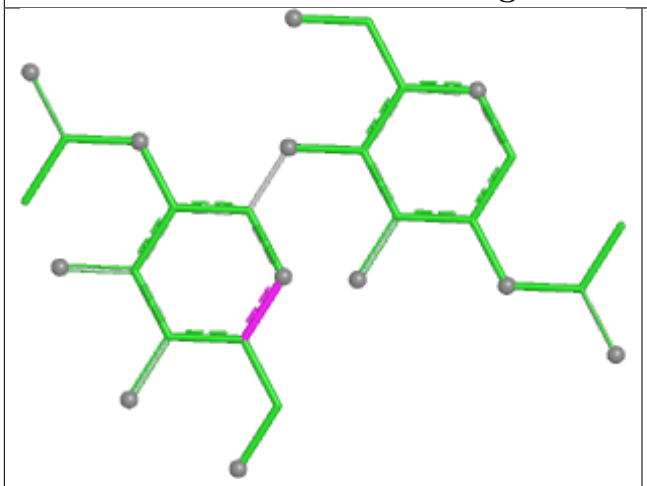


Rings

Oligosaccharide Chain S



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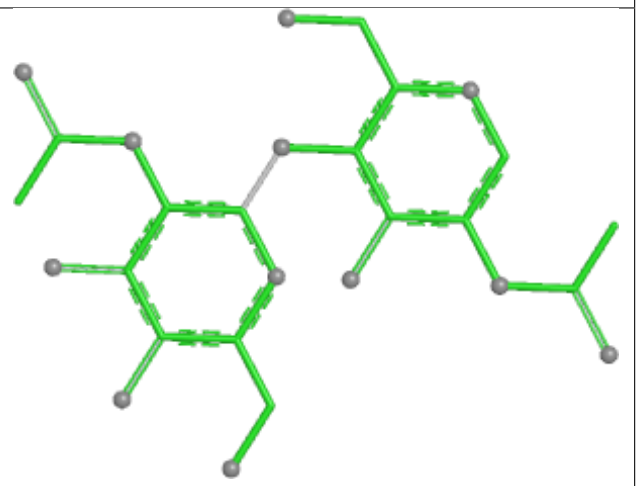
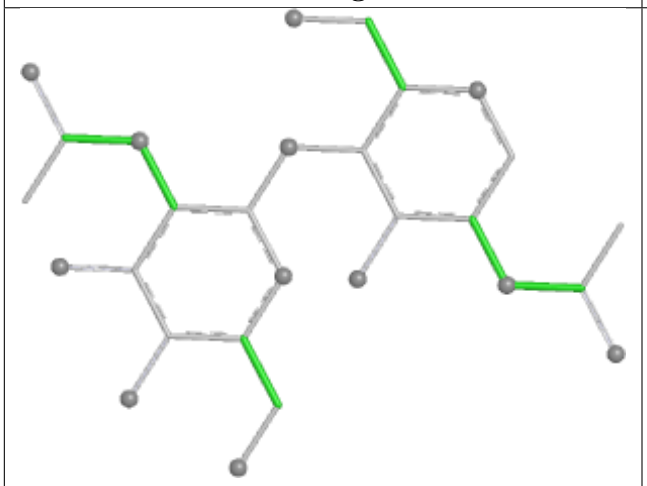
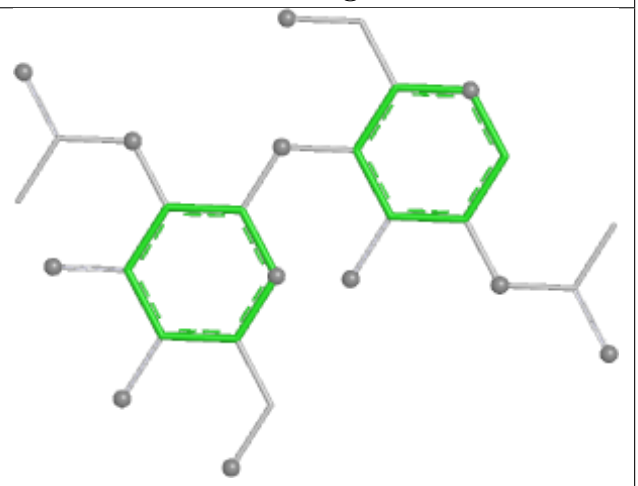


Bond angles

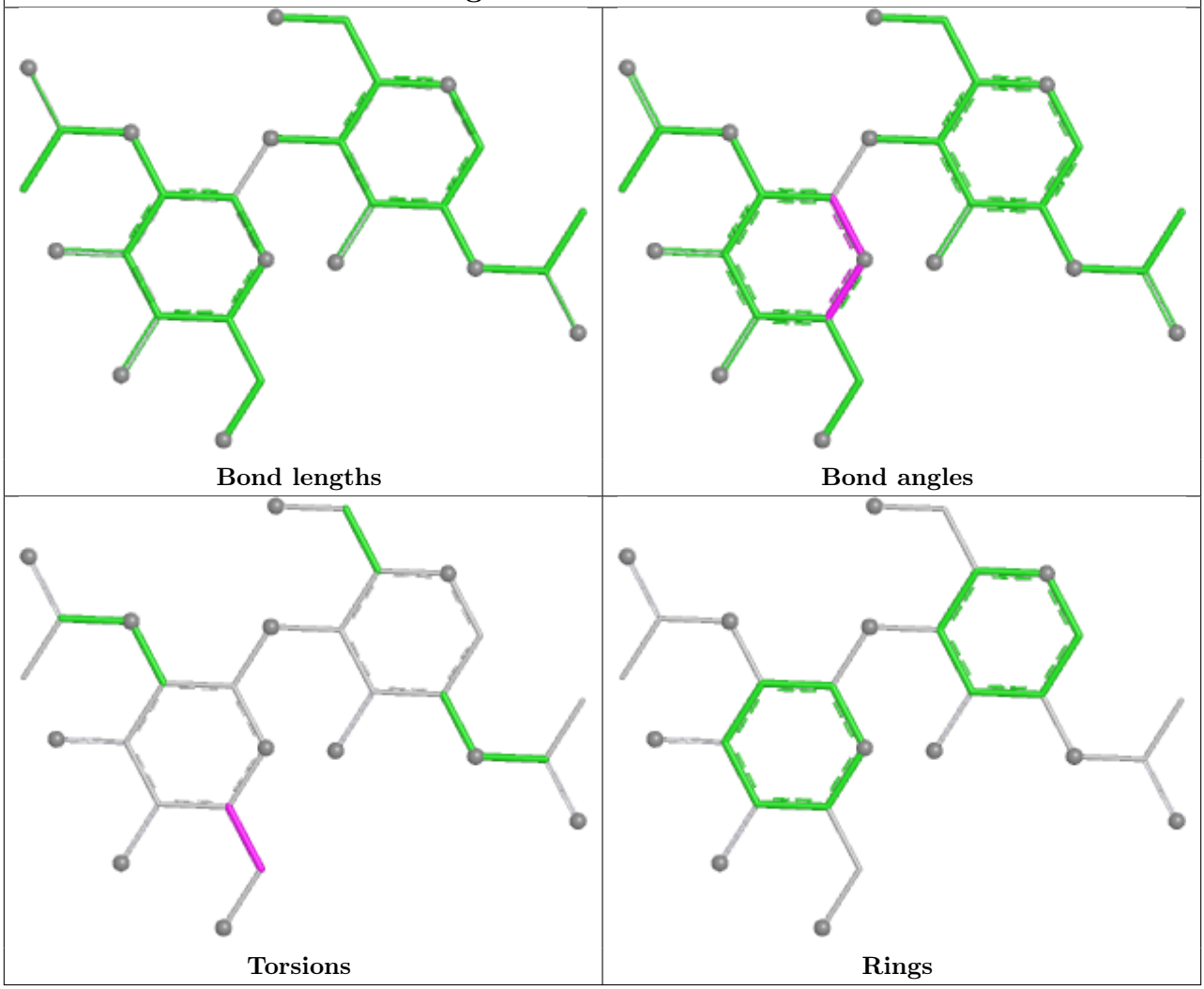


Torsions

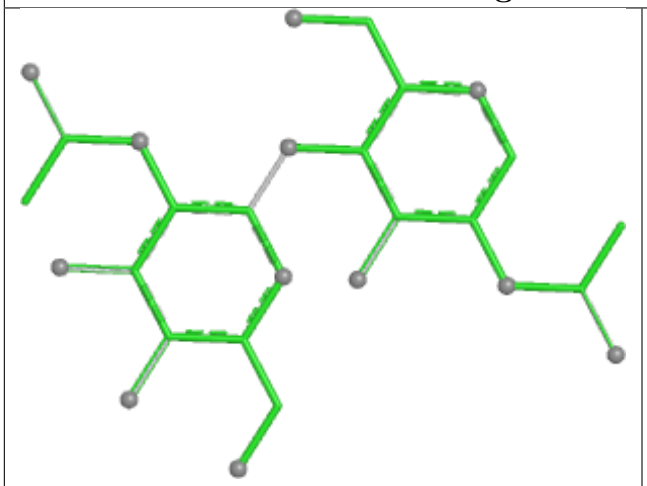


Rings

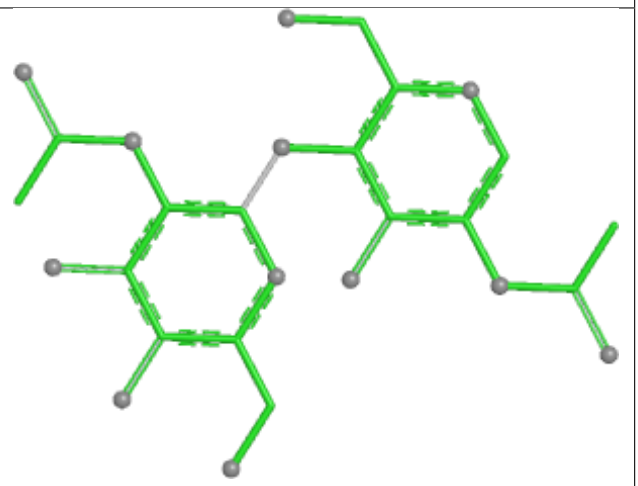
Oligosaccharide Chain T



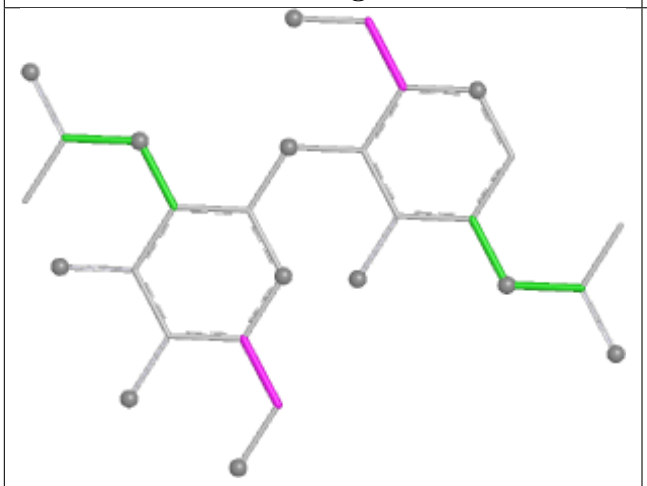
Oligosaccharide Chain U



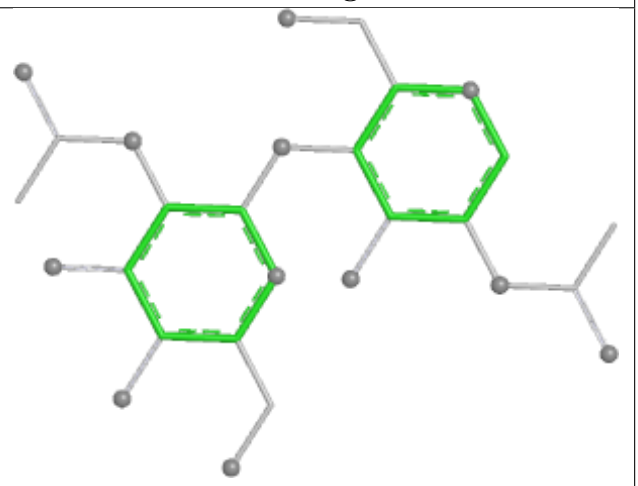
Bond lengths



Bond angles

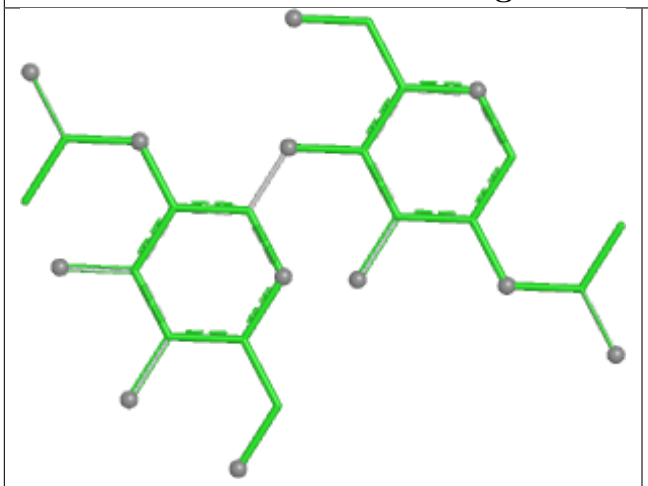


Torsions

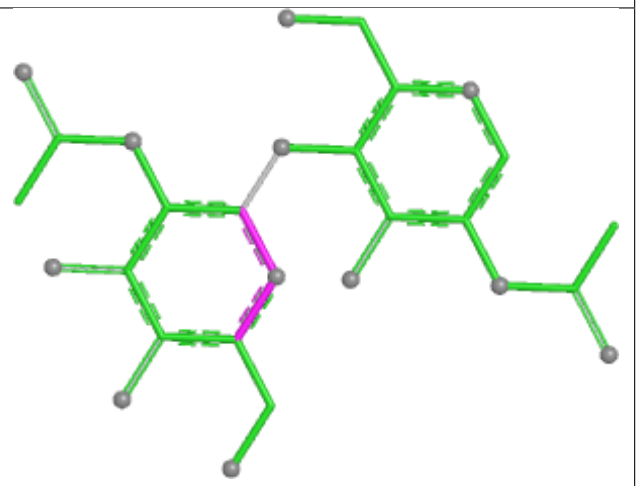


Rings

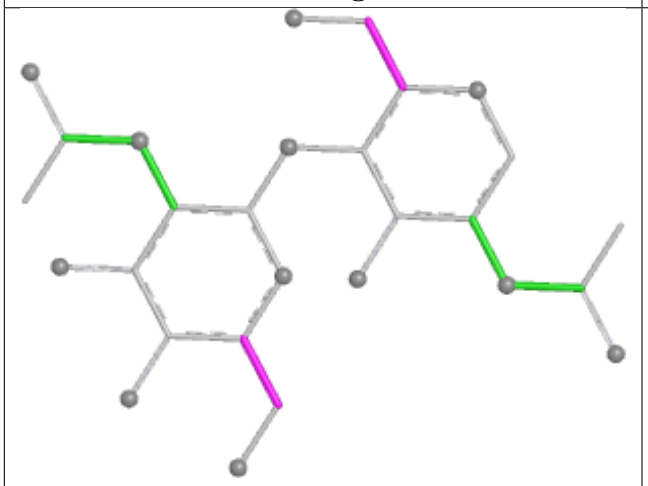
Oligosaccharide Chain V



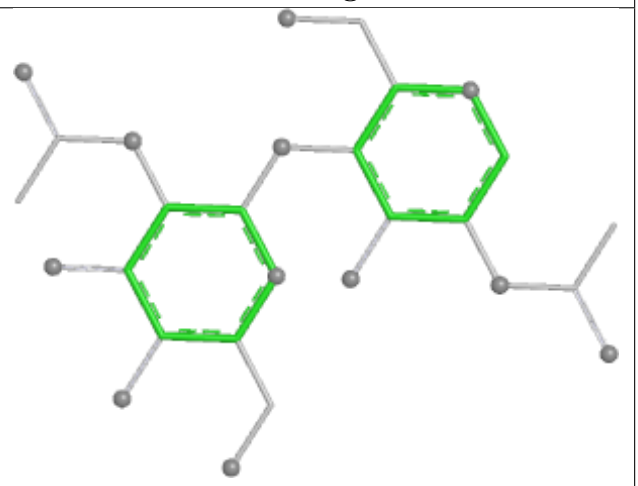
Bond lengths



Bond angles

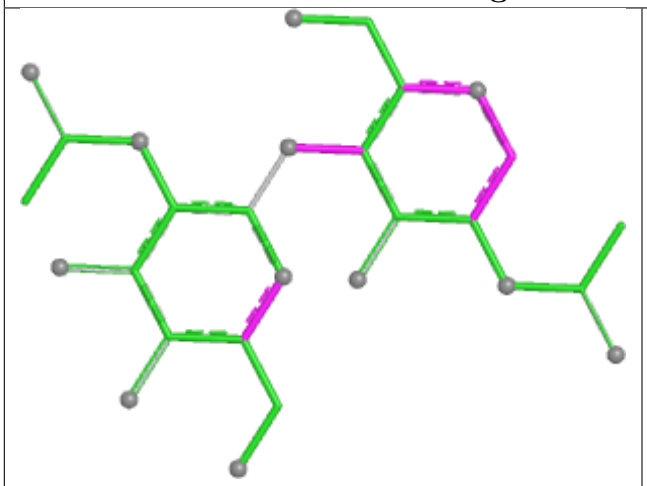


Torsions

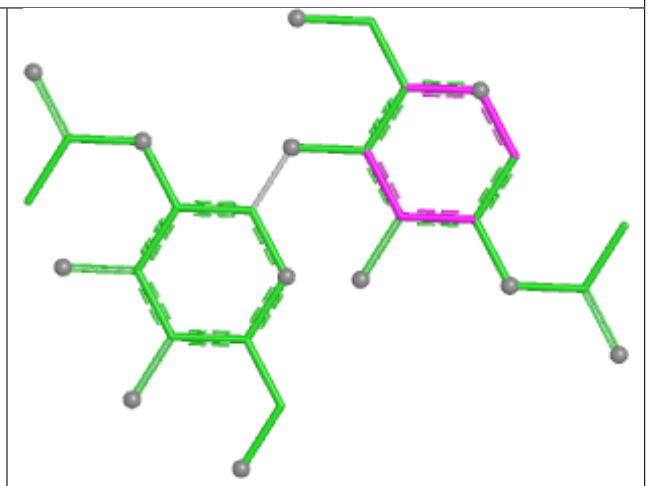


Rings

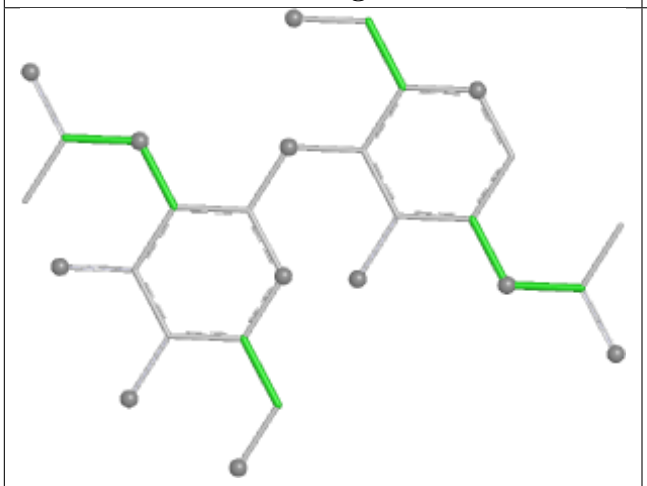
Oligosaccharide Chain W



Bond lengths



Bond angles



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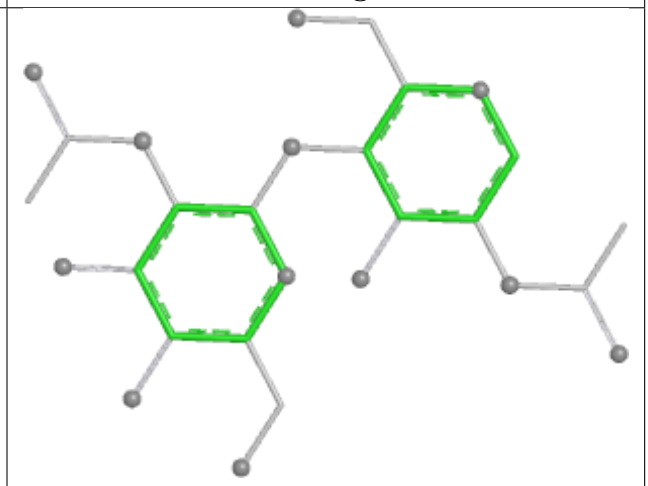
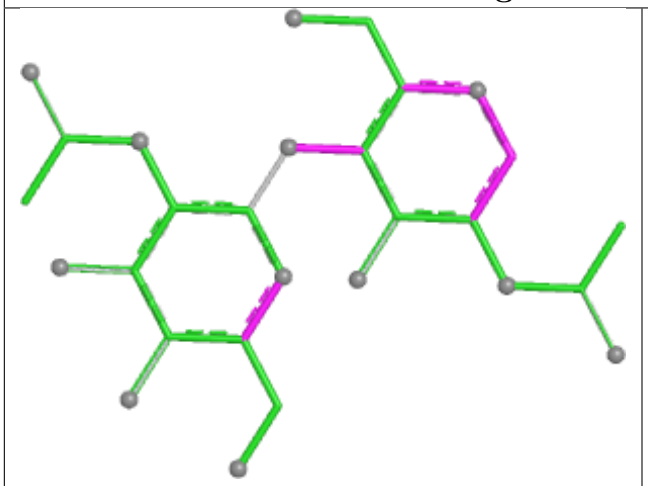


Rings

Oligosaccharide Chain X



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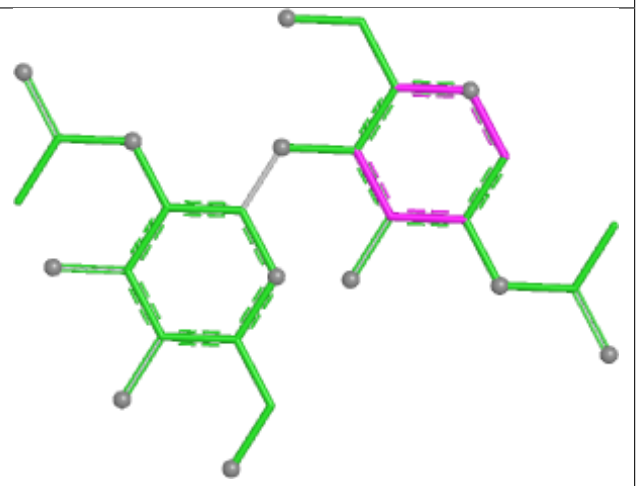
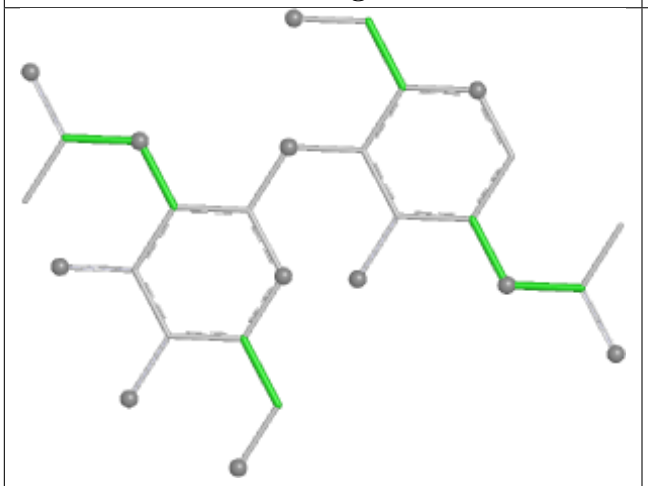


Bond angles



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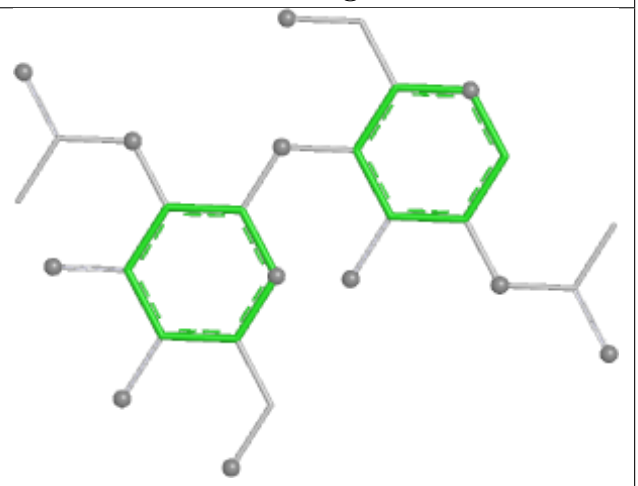
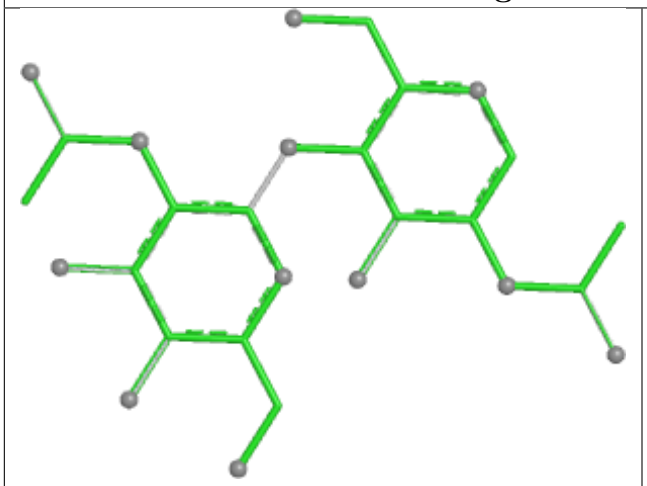


Rings

Oligosaccharide Chain Y



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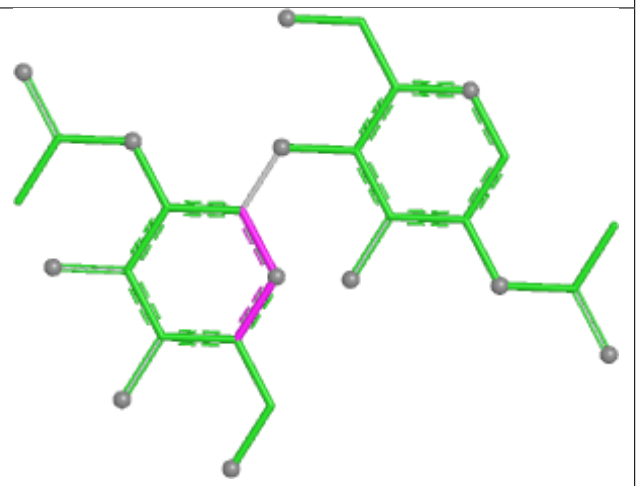

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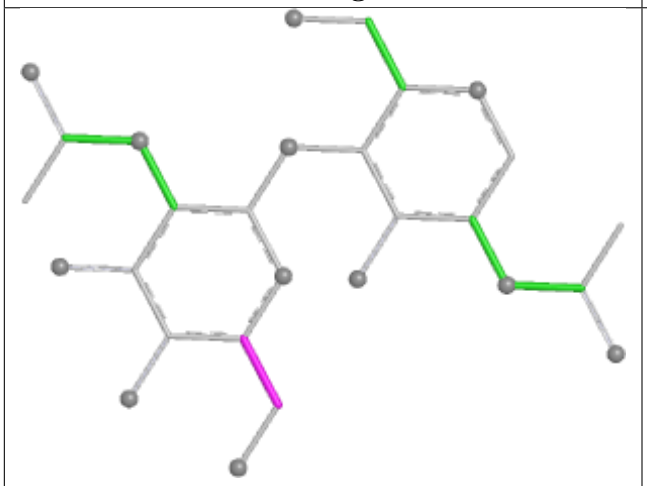

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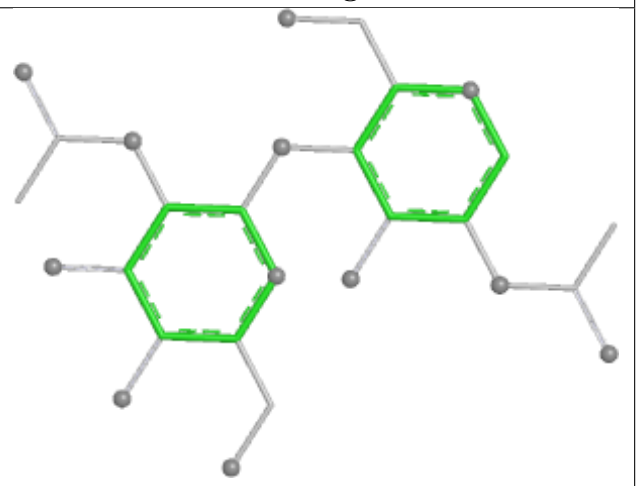
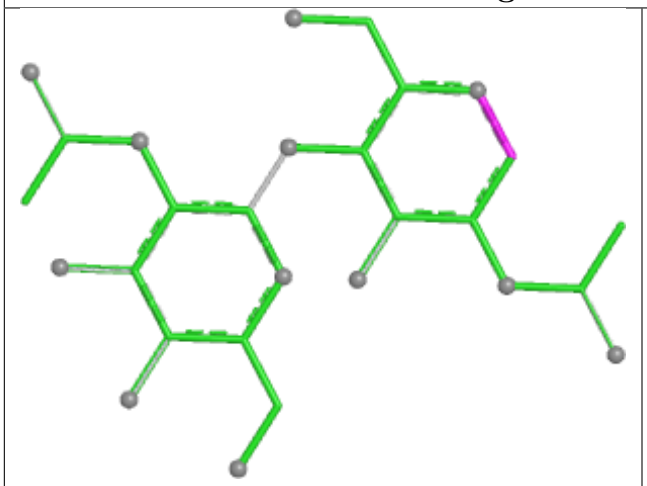
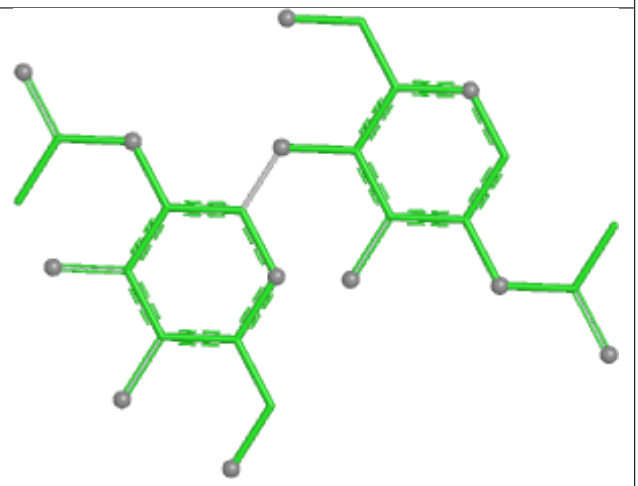


Rings

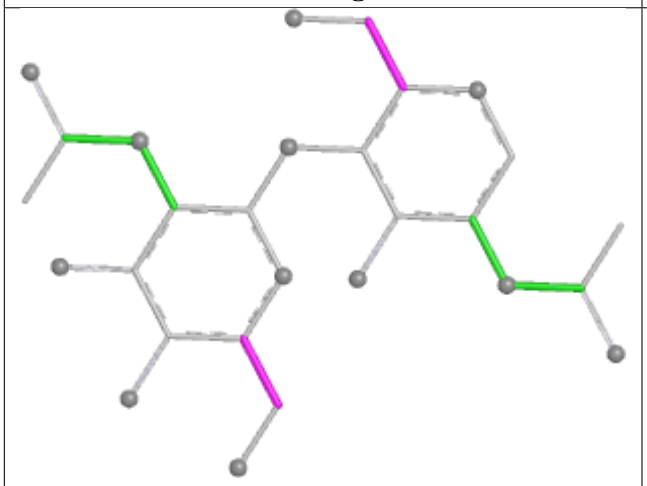
Oligosaccharide Chain Z



Bond lengths



Bond angles



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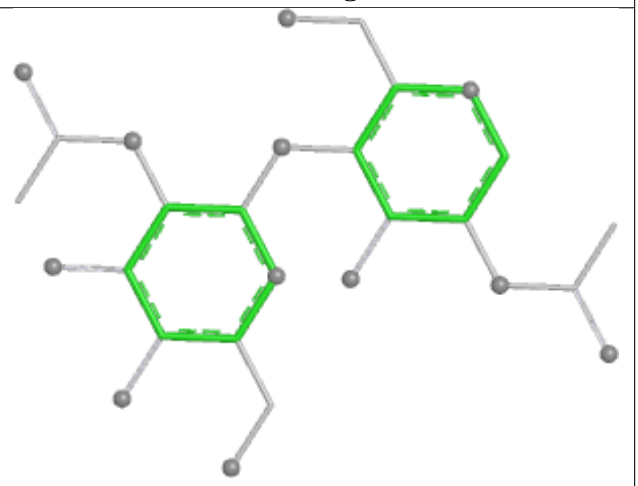
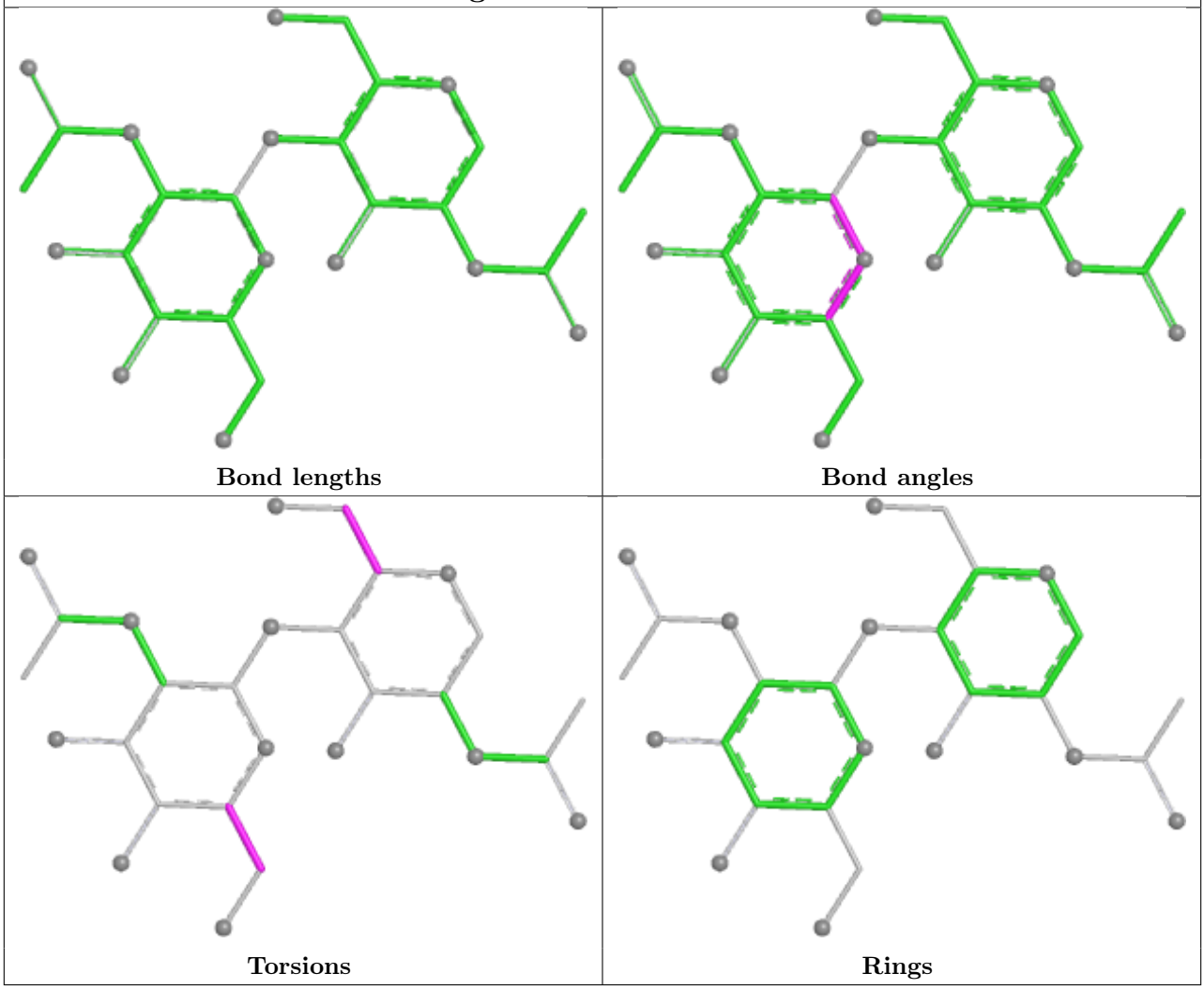
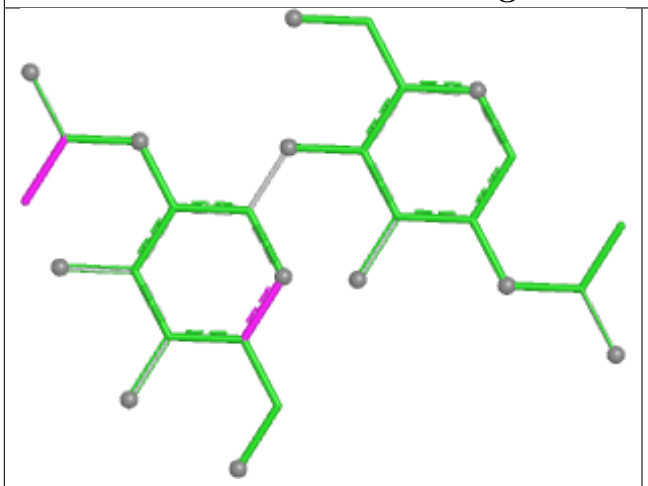


Rings

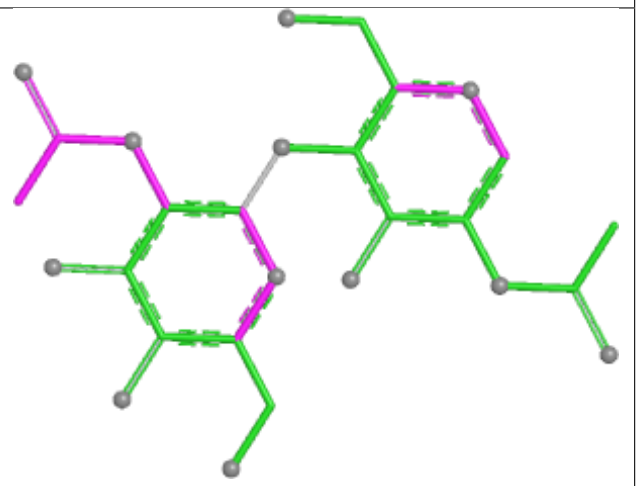
Oligosaccharide Chain a



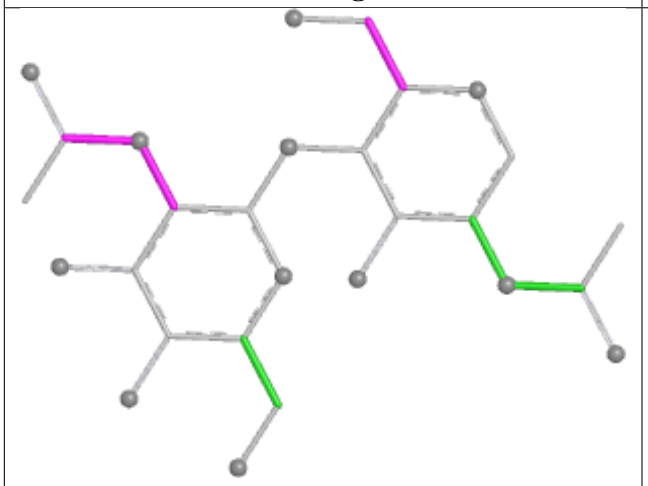
Oligosaccharide Chain b



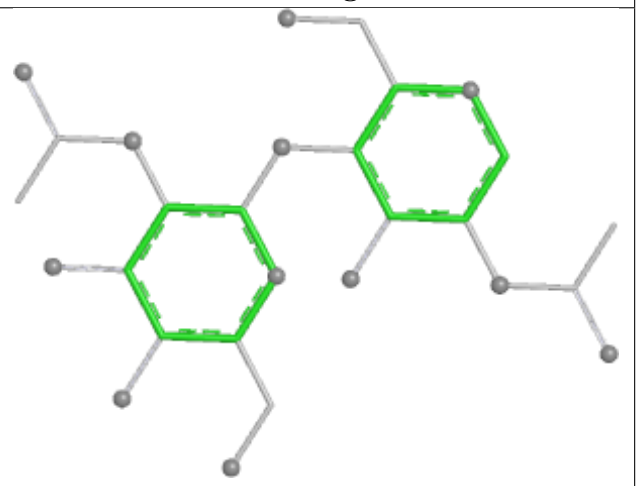
Bond lengths



Bond angles

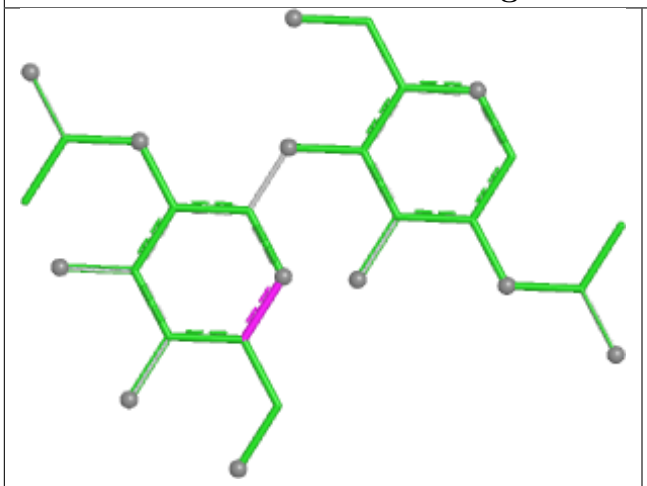


Torsions

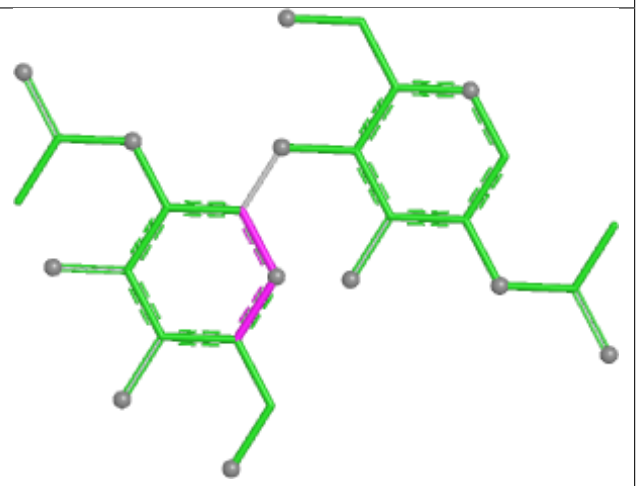


Rings

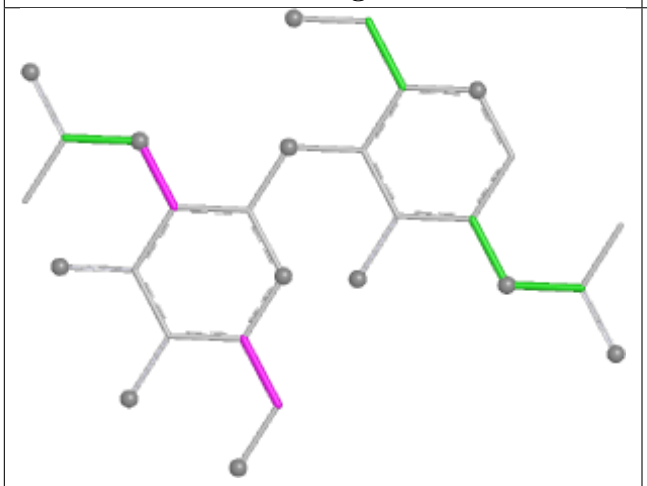
Oligosaccharide Chain c



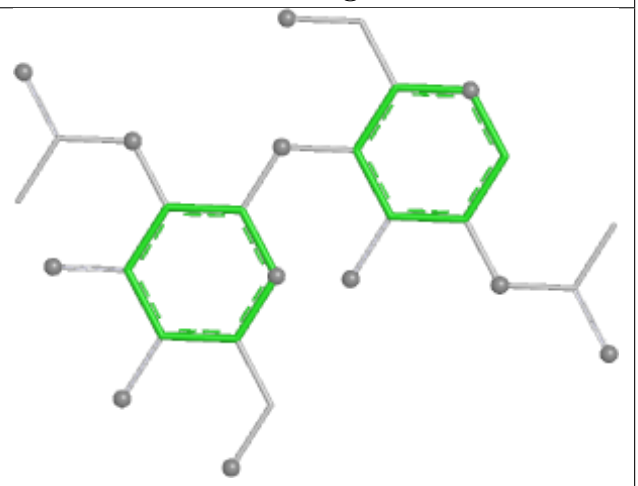
Bond lengths



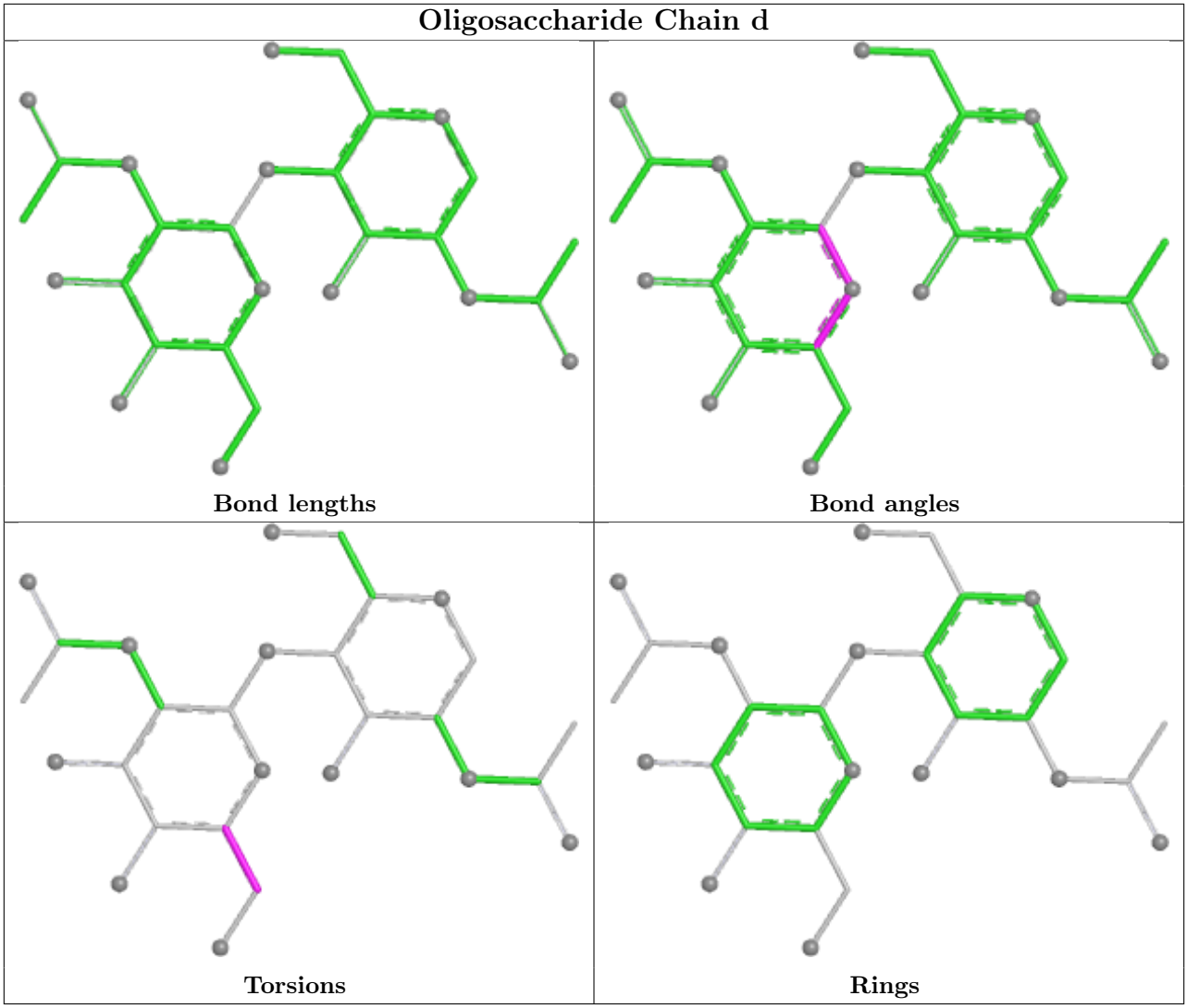
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

42 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	NAG	A	1309	1	14,14,15	1.69	2 (14%)	17,19,21	0.71	0
4	NAG	C	1308	1	14,14,15	1.30	2 (14%)	17,19,21	0.91	0
4	NAG	B	1309	1	14,14,15	1.39	3 (21%)	17,19,21	0.87	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	NAG	A	1302	-	14,14,15	1.95	3 (21%)	17,19,21	0.91	1 (5%)
4	NAG	B	1304	-	14,14,15	1.60	2 (14%)	17,19,21	0.71	0
4	NAG	E	701	2	14,14,15	1.27	2 (14%)	17,19,21	0.90	0
4	NAG	C	1302	-	14,14,15	1.64	2 (14%)	17,19,21	0.73	0
4	NAG	A	1301	-	14,14,15	1.62	2 (14%)	17,19,21	0.65	0
4	NAG	B	1305	1	14,14,15	1.19	2 (14%)	17,19,21	0.77	0
4	NAG	B	1311	1	14,14,15	1.23	2 (14%)	17,19,21	0.60	0
4	NAG	A	1310	1	14,14,15	1.58	2 (14%)	17,19,21	0.71	0
4	NAG	C	1312	-	14,14,15	1.76	2 (14%)	17,19,21	1.26	1 (5%)
4	NAG	B	1310	1	14,14,15	1.22	2 (14%)	17,19,21	0.83	1 (5%)
4	NAG	C	1313	-	14,14,15	1.63	2 (14%)	17,19,21	1.01	1 (5%)
4	NAG	B	1307	-	14,14,15	1.60	2 (14%)	17,19,21	0.66	0
4	NAG	C	1303	-	14,14,15	1.66	2 (14%)	17,19,21	0.68	0
4	NAG	A	1308	-	14,14,15	1.59	2 (14%)	17,19,21	0.72	0
4	NAG	A	1305	1	14,14,15	1.44	3 (21%)	17,19,21	0.74	0
4	NAG	A	1313	1	14,14,15	1.28	2 (14%)	17,19,21	0.98	1 (5%)
4	NAG	C	1301	-	14,14,15	1.61	2 (14%)	17,19,21	0.67	0
4	NAG	F	701	-	14,14,15	0.17	0	17,19,21	0.48	0
4	NAG	B	1308	1	14,14,15	1.62	2 (14%)	17,19,21	0.63	0
4	NAG	B	1312	-	14,14,15	1.57	2 (14%)	17,19,21	0.70	0
4	NAG	A	1303	-	14,14,15	1.64	2 (14%)	17,19,21	0.68	0
4	NAG	C	1306	-	14,14,15	1.73	3 (21%)	17,19,21	0.91	1 (5%)
4	NAG	C	1309	-	14,14,15	1.69	2 (14%)	17,19,21	0.72	0
4	NAG	B	1313	-	14,14,15	1.67	3 (21%)	17,19,21	0.73	0
4	NAG	C	1304	1	14,14,15	1.41	3 (21%)	17,19,21	1.26	1 (5%)
4	NAG	A	1312	-	14,14,15	1.59	2 (14%)	17,19,21	0.70	0
4	NAG	C	1310	1	14,14,15	1.53	3 (21%)	17,19,21	0.65	0
4	NAG	C	1311	-	14,14,15	1.17	2 (14%)	17,19,21	1.20	1 (5%)
4	NAG	A	1306	-	14,14,15	1.70	2 (14%)	17,19,21	0.90	1 (5%)
4	NAG	A	1304	1	14,14,15	1.64	2 (14%)	17,19,21	0.69	0
4	NAG	C	1307	-	14,14,15	1.60	2 (14%)	17,19,21	0.66	0
4	NAG	B	1302	-	14,14,15	1.91	3 (21%)	17,19,21	0.91	0
4	NAG	B	1303	-	14,14,15	1.68	2 (14%)	17,19,21	0.67	0
4	NAG	A	1307	-	14,14,15	1.64	2 (14%)	17,19,21	0.68	0
4	NAG	C	1305	1	14,14,15	1.65	2 (14%)	17,19,21	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	NAG	A	1311	1	14,14,15	1.47	2 (14%)	17,19,21	0.77	0
4	NAG	B	1306	-	14,14,15	1.70	2 (14%)	17,19,21	0.91	1 (5%)
4	NAG	B	1301	-	14,14,15	1.64	2 (14%)	17,19,21	0.67	0
4	NAG	D	701	2	14,14,15	1.40	3 (21%)	17,19,21	1.06	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	1309	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1308	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1309	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1302	-	-	0/6/23/26	0/1/1/1
4	NAG	B	1304	-	-	0/6/23/26	0/1/1/1
4	NAG	E	701	2	-	0/6/23/26	0/1/1/1
4	NAG	C	1302	-	-	0/6/23/26	0/1/1/1
4	NAG	A	1301	-	-	0/6/23/26	0/1/1/1
4	NAG	B	1305	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1311	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1310	1	-	1/6/23/26	0/1/1/1
4	NAG	C	1312	-	-	0/6/23/26	0/1/1/1
4	NAG	B	1310	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1313	-	-	0/6/23/26	0/1/1/1
4	NAG	B	1307	-	-	0/6/23/26	0/1/1/1
4	NAG	C	1303	-	-	0/6/23/26	0/1/1/1
4	NAG	A	1308	-	-	0/6/23/26	0/1/1/1
4	NAG	A	1305	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1313	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1301	-	-	0/6/23/26	0/1/1/1
4	NAG	F	701	-	-	0/6/23/26	0/1/1/1
4	NAG	B	1308	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1312	-	-	0/6/23/26	0/1/1/1
4	NAG	A	1303	-	-	0/6/23/26	0/1/1/1
4	NAG	C	1306	-	-	2/6/23/26	0/1/1/1
4	NAG	C	1309	-	-	0/6/23/26	0/1/1/1
4	NAG	B	1313	-	-	0/6/23/26	0/1/1/1
4	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1312	-	-	0/6/23/26	0/1/1/1
4	NAG	C	1310	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	C	1311	-	-	1/6/23/26	0/1/1/1
4	NAG	A	1306	-	-	2/6/23/26	0/1/1/1
4	NAG	A	1304	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1307	-	-	0/6/23/26	0/1/1/1
4	NAG	B	1302	-	-	0/6/23/26	0/1/1/1
4	NAG	B	1303	-	-	0/6/23/26	0/1/1/1
4	NAG	A	1307	-	-	0/6/23/26	0/1/1/1
4	NAG	C	1305	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1311	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1306	-	-	2/6/23/26	0/1/1/1
4	NAG	B	1301	-	-	0/6/23/26	0/1/1/1
4	NAG	D	701	2	-	0/6/23/26	0/1/1/1

All (91) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1302	NAG	C1-C2	5.67	1.60	1.52
4	B	1302	NAG	C1-C2	5.45	1.59	1.52
4	C	1309	NAG	C1-C2	4.86	1.59	1.52
4	A	1309	NAG	C1-C2	4.82	1.58	1.52
4	C	1305	NAG	C1-C2	4.77	1.58	1.52
4	B	1303	NAG	C1-C2	4.73	1.58	1.52
4	C	1303	NAG	C1-C2	4.63	1.58	1.52
4	B	1308	NAG	C1-C2	4.62	1.58	1.52
4	B	1301	NAG	C1-C2	4.60	1.58	1.52
4	A	1307	NAG	C1-C2	4.60	1.58	1.52
4	A	1308	NAG	C1-C2	4.60	1.58	1.52
4	C	1302	NAG	C1-C2	4.59	1.58	1.52
4	B	1313	NAG	C1-C2	4.59	1.58	1.52
4	A	1303	NAG	C1-C2	4.58	1.58	1.52
4	A	1306	NAG	C1-C2	4.57	1.58	1.52
4	C	1306	NAG	C1-C2	4.56	1.58	1.52
4	C	1312	NAG	C1-C2	4.55	1.58	1.52
4	A	1312	NAG	C1-C2	4.54	1.58	1.52
4	A	1304	NAG	C1-C2	4.54	1.58	1.52
4	C	1313	NAG	C1-C2	4.53	1.58	1.52
4	B	1306	NAG	C1-C2	4.49	1.58	1.52
4	B	1312	NAG	C1-C2	4.46	1.58	1.52
4	A	1301	NAG	C1-C2	4.44	1.58	1.52
4	A	1310	NAG	C1-C2	4.43	1.58	1.52
4	C	1307	NAG	C1-C2	4.43	1.58	1.52
4	C	1301	NAG	C1-C2	4.42	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1307	NAG	C1-C2	4.41	1.58	1.52
4	B	1304	NAG	C1-C2	4.38	1.58	1.52
4	A	1311	NAG	C1-C2	4.08	1.57	1.52
4	C	1310	NAG	C1-C2	3.50	1.57	1.52
4	D	701	NAG	O5-C5	3.33	1.49	1.43
4	C	1312	NAG	O5-C5	3.31	1.49	1.43
4	C	1304	NAG	O5-C5	3.15	1.49	1.43
4	B	1309	NAG	O5-C5	3.02	1.49	1.43
4	A	1302	NAG	O5-C5	2.96	1.49	1.43
4	B	1302	NAG	O5-C5	2.89	1.49	1.43
4	A	1305	NAG	C1-C2	2.85	1.56	1.52
4	A	1305	NAG	O5-C5	2.79	1.48	1.43
4	E	701	NAG	O5-C5	2.79	1.48	1.43
4	C	1308	NAG	O5-C5	2.76	1.48	1.43
4	C	1306	NAG	O5-C5	2.75	1.48	1.43
4	B	1306	NAG	O5-C5	2.74	1.48	1.43
4	A	1306	NAG	O5-C5	2.73	1.48	1.43
4	A	1313	NAG	O5-C5	2.73	1.48	1.43
4	C	1311	NAG	O5-C5	2.71	1.48	1.43
4	A	1304	NAG	O5-C5	2.64	1.48	1.43
4	B	1305	NAG	O5-C5	2.64	1.48	1.43
4	A	1303	NAG	O5-C5	2.58	1.48	1.43
4	B	1303	NAG	O5-C5	2.56	1.48	1.43
4	B	1311	NAG	O5-C5	2.54	1.48	1.43
4	D	701	NAG	O5-C1	2.52	1.47	1.43
4	B	1313	NAG	O5-C5	2.51	1.48	1.43
4	B	1304	NAG	O5-C5	2.51	1.48	1.43
4	C	1303	NAG	O5-C5	2.50	1.48	1.43
4	C	1308	NAG	C1-C2	2.50	1.55	1.52
4	B	1307	NAG	O5-C5	2.49	1.48	1.43
4	C	1305	NAG	O5-C5	2.49	1.48	1.43
4	C	1310	NAG	O5-C1	2.47	1.47	1.43
4	A	1313	NAG	C1-C2	2.47	1.55	1.52
4	C	1307	NAG	O5-C5	2.47	1.48	1.43
4	C	1310	NAG	O5-C5	2.45	1.48	1.43
4	B	1309	NAG	C1-C2	2.45	1.55	1.52
4	A	1308	NAG	O5-C5	2.43	1.48	1.43
4	C	1313	NAG	O5-C5	2.43	1.48	1.43
4	A	1305	NAG	O5-C1	2.42	1.47	1.43
4	A	1307	NAG	O5-C5	2.42	1.48	1.43
4	A	1310	NAG	O5-C5	2.42	1.48	1.43
4	A	1301	NAG	O5-C5	2.42	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1310	NAG	O5-C5	2.41	1.48	1.43
4	B	1308	NAG	O5-C5	2.40	1.48	1.43
4	A	1309	NAG	O5-C5	2.40	1.48	1.43
4	B	1312	NAG	O5-C5	2.40	1.48	1.43
4	C	1301	NAG	O5-C5	2.40	1.48	1.43
4	C	1304	NAG	C1-C2	2.40	1.55	1.52
4	B	1301	NAG	O5-C5	2.38	1.48	1.43
4	C	1309	NAG	O5-C5	2.36	1.48	1.43
4	C	1302	NAG	O5-C5	2.35	1.48	1.43
4	A	1312	NAG	O5-C5	2.35	1.48	1.43
4	B	1310	NAG	C1-C2	2.26	1.55	1.52
4	B	1311	NAG	C1-C2	2.25	1.55	1.52
4	B	1302	NAG	O5-C1	2.22	1.47	1.43
4	A	1311	NAG	O5-C5	2.21	1.47	1.43
4	A	1302	NAG	O5-C1	2.16	1.47	1.43
4	C	1304	NAG	O5-C1	2.14	1.47	1.43
4	B	1309	NAG	O5-C1	2.11	1.47	1.43
4	B	1313	NAG	C3-C2	2.08	1.56	1.52
4	E	701	NAG	C1-C2	2.08	1.55	1.52
4	C	1311	NAG	C1-C2	2.06	1.55	1.52
4	C	1306	NAG	C4-C5	2.06	1.57	1.53
4	B	1305	NAG	C1-C2	2.06	1.55	1.52
4	D	701	NAG	C1-C2	2.06	1.55	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	1304	NAG	C1-O5-C5	4.35	118.01	112.19
4	C	1311	NAG	C1-O5-C5	4.26	117.90	112.19
4	C	1312	NAG	C1-O5-C5	4.20	117.81	112.19
4	C	1313	NAG	C1-O5-C5	2.89	116.06	112.19
4	A	1313	NAG	C1-O5-C5	2.77	115.89	112.19
4	B	1310	NAG	C1-O5-C5	2.64	115.72	112.19
4	D	701	NAG	C1-O5-C5	2.60	115.67	112.19
4	C	1306	NAG	O5-C1-C2	-2.43	107.54	111.29
4	B	1306	NAG	O5-C1-C2	-2.42	107.55	111.29
4	A	1306	NAG	O5-C1-C2	-2.36	107.64	111.29
4	B	1309	NAG	C1-O5-C5	2.19	115.11	112.19
4	A	1302	NAG	C2-N2-C7	2.07	125.67	122.90

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1306	NAG	O5-C5-C6-O6
4	B	1306	NAG	O5-C5-C6-O6
4	C	1306	NAG	O5-C5-C6-O6
4	A	1306	NAG	C4-C5-C6-O6
4	B	1306	NAG	C4-C5-C6-O6
4	C	1306	NAG	C4-C5-C6-O6
4	A	1310	NAG	C1-C2-N2-C7
4	C	1311	NAG	C1-C2-N2-C7

There are no ring outliers.

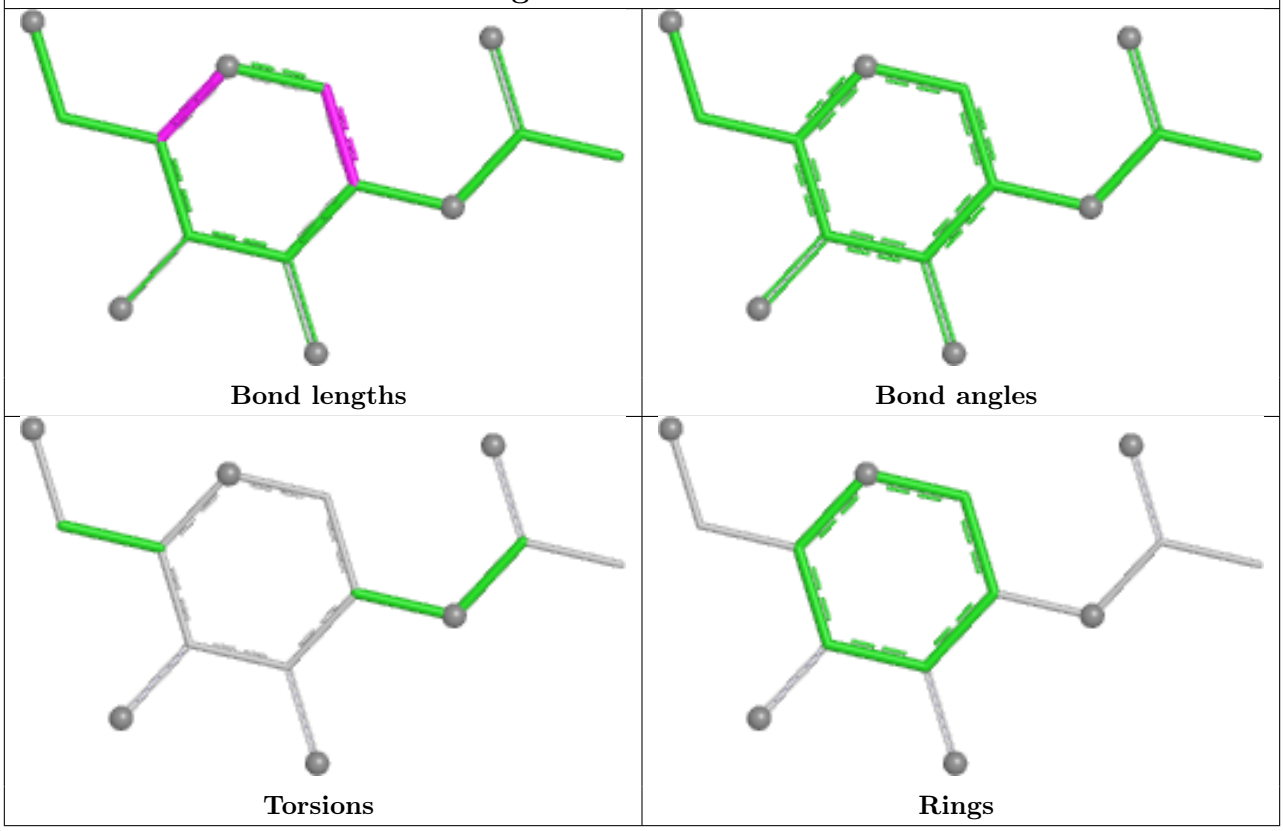
25 monomers are involved in 77 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1302	NAG	3	0
4	B	1304	NAG	2	0
4	C	1302	NAG	1	0
4	A	1301	NAG	6	0
4	C	1312	NAG	3	0
4	C	1313	NAG	4	0
4	B	1307	NAG	3	0
4	C	1303	NAG	3	0
4	A	1308	NAG	6	0
4	F	701	NAG	2	0
4	B	1312	NAG	6	0
4	A	1303	NAG	2	0
4	C	1306	NAG	3	0
4	B	1313	NAG	6	0
4	A	1312	NAG	3	0
4	C	1310	NAG	1	0
4	C	1311	NAG	2	0
4	A	1306	NAG	5	0
4	C	1307	NAG	3	0
4	B	1302	NAG	2	0
4	B	1303	NAG	2	0
4	A	1307	NAG	4	0
4	A	1311	NAG	1	0
4	B	1306	NAG	2	0
4	B	1301	NAG	2	0

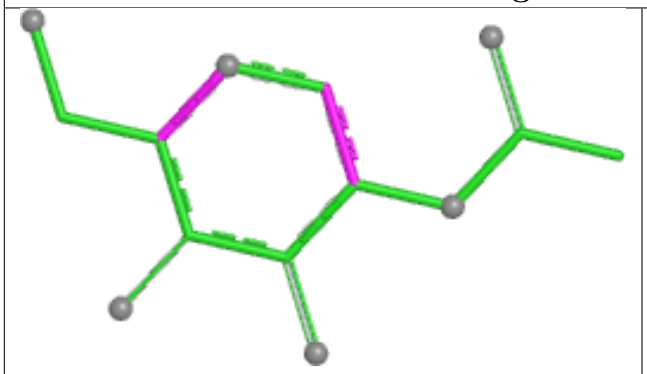
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is

within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

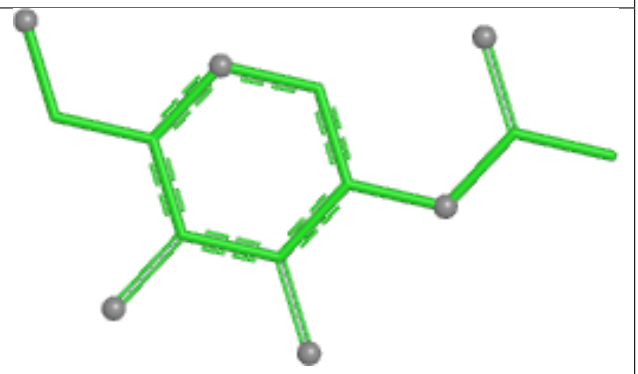
Ligand NAG A 1309



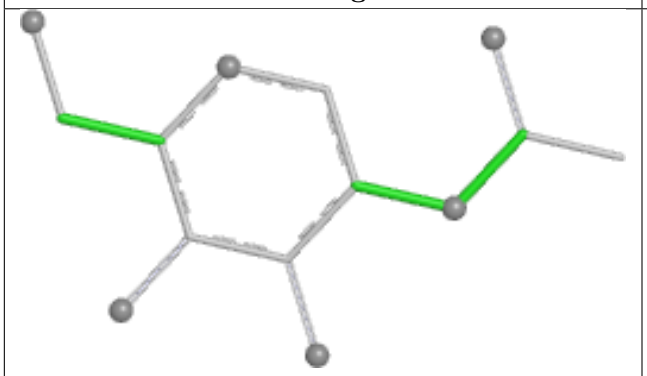
Ligand NAG C 1308



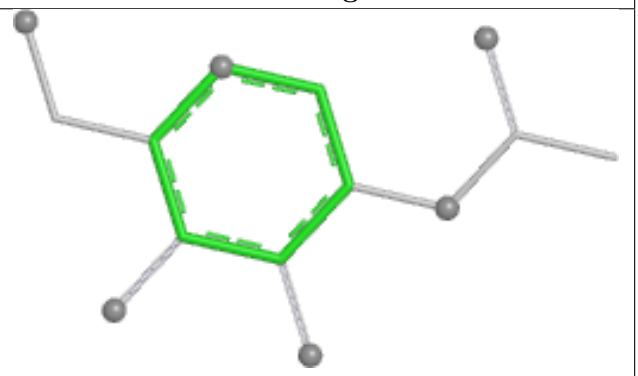
Bond lengths



Bond angles

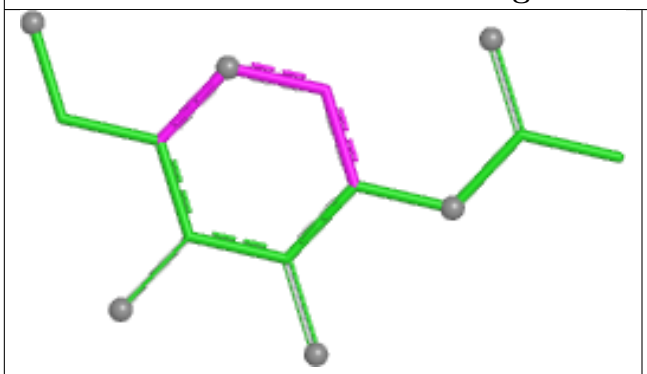


Torsions

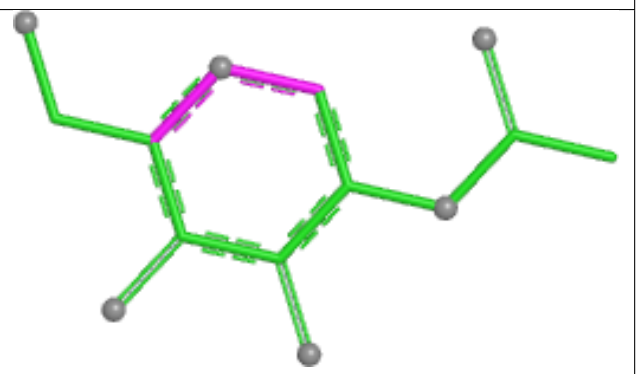


Rings

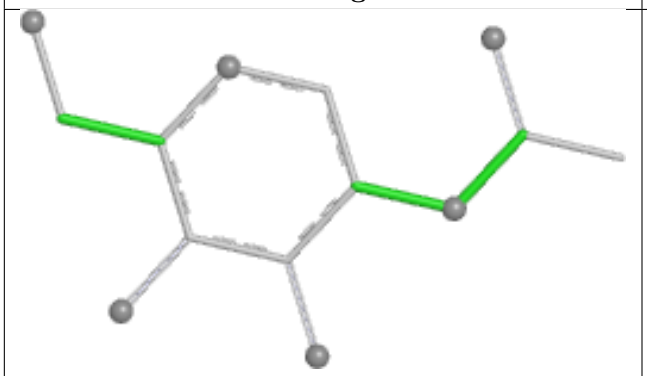
Ligand NAG B 1309



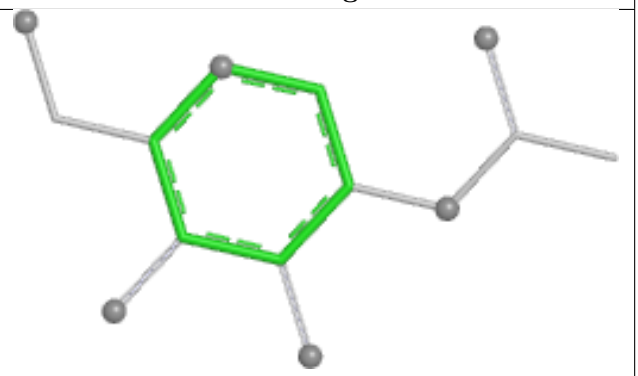
Bond lengths



Bond angles

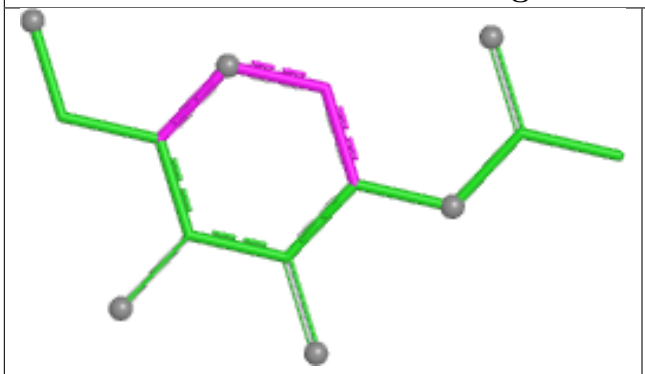


Torsions

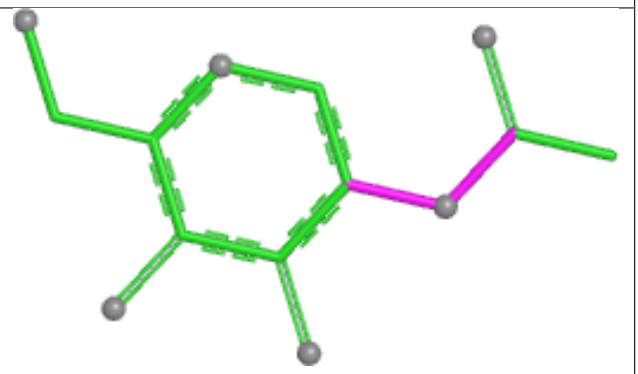


Rings

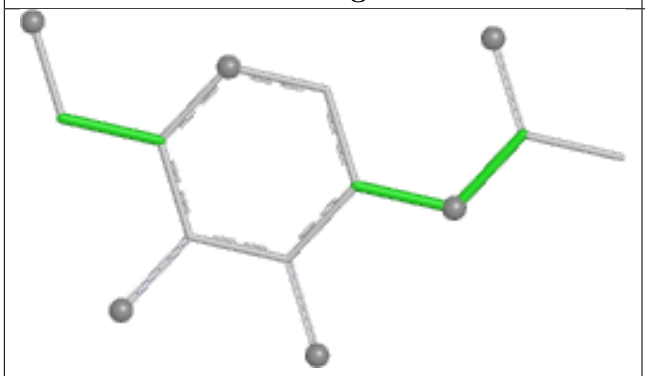
Ligand NAG A 1302



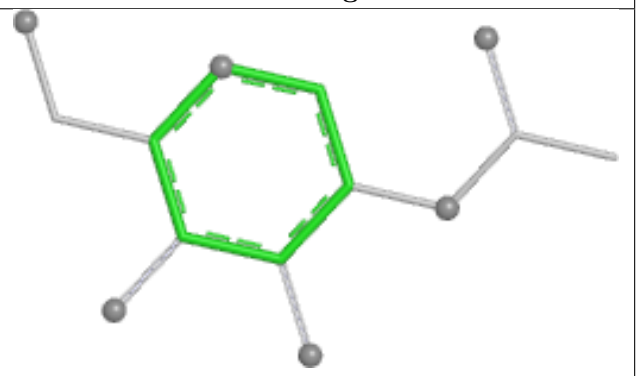
Bond lengths



Bond angles

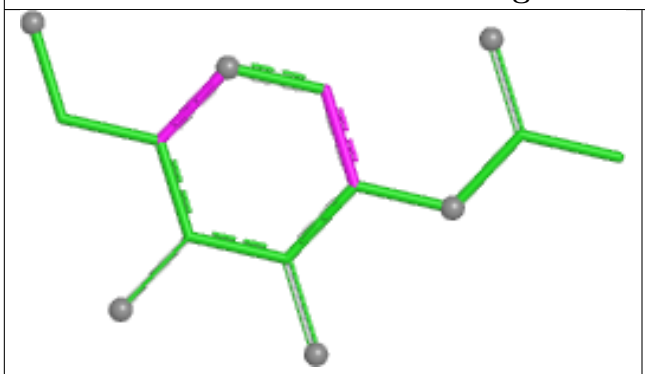


Torsions

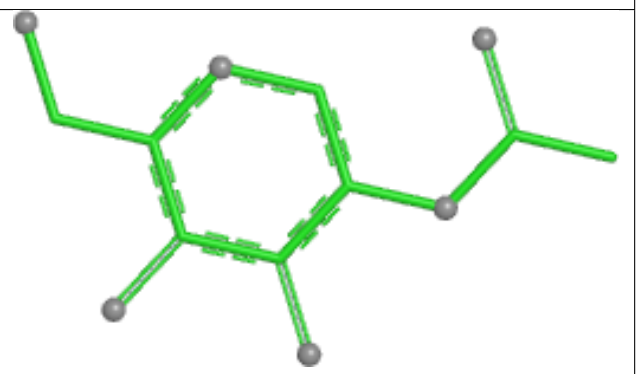


Rings

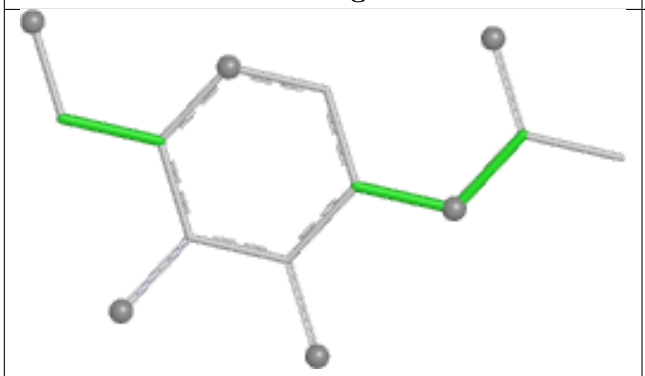
Ligand NAG B 1304



Bond lengths



Bond angles



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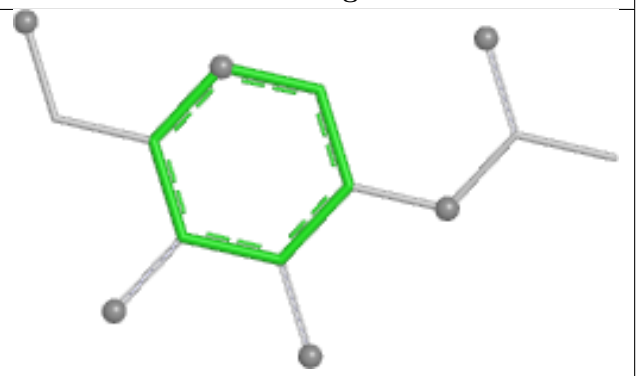
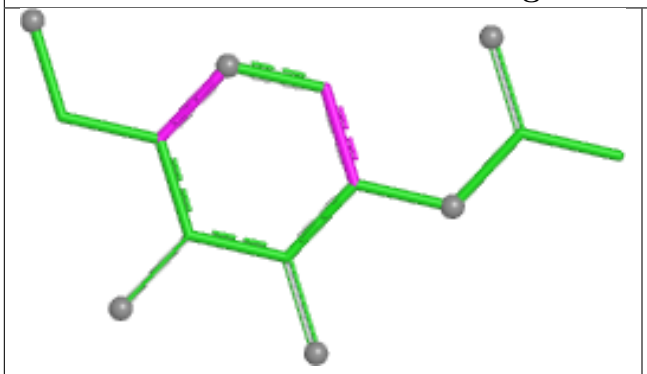


Rings

Ligand NAG E 701



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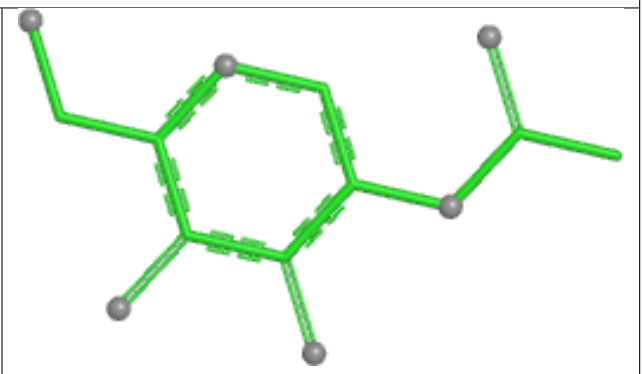
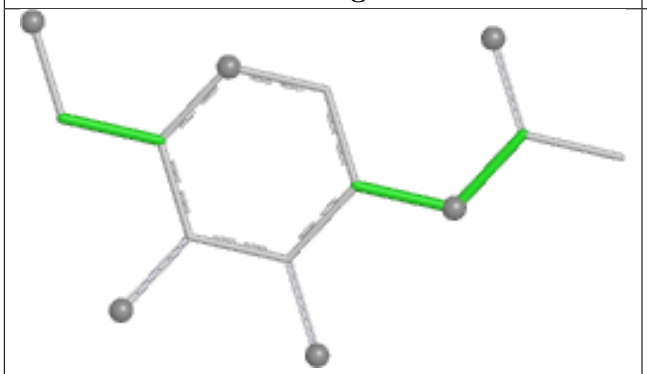


Bond angles



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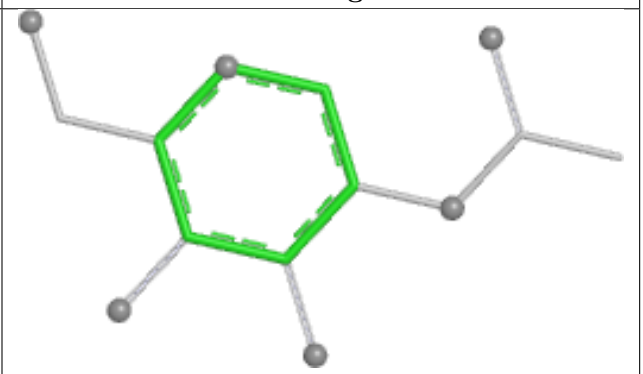
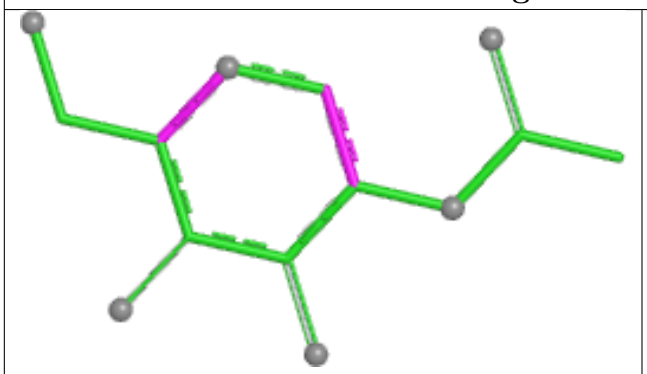


Rings

Ligand NAG C 1302



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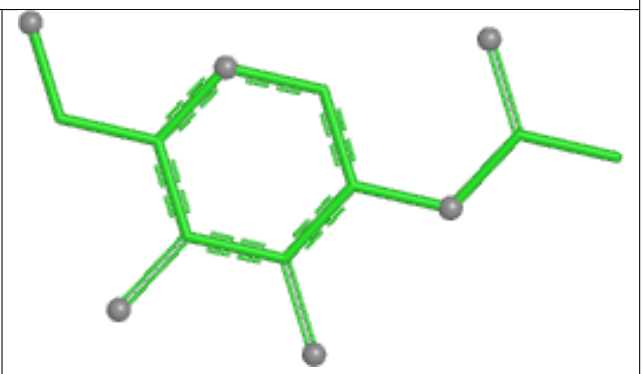
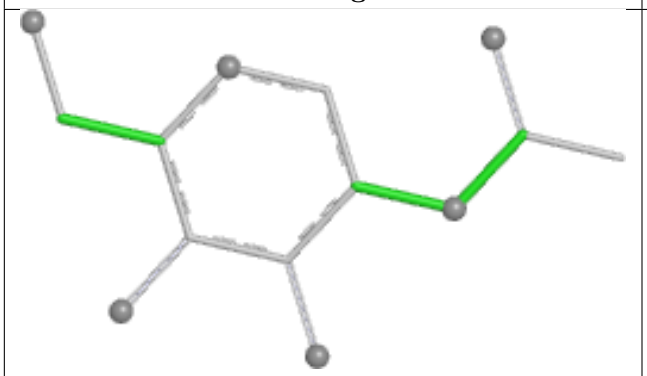


Bond angles



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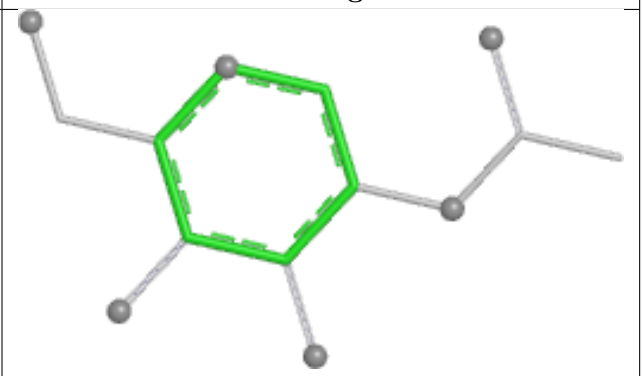
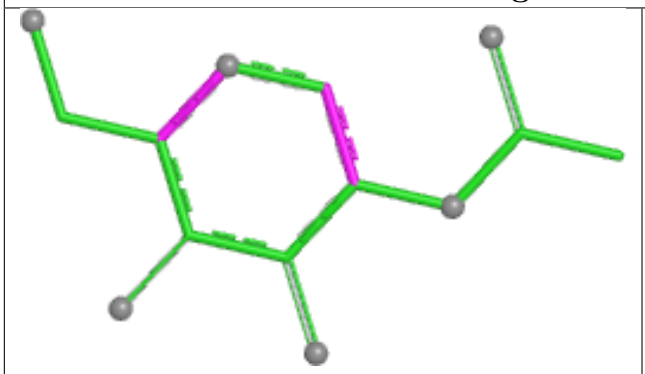


Rings

Ligand NAG A 1301



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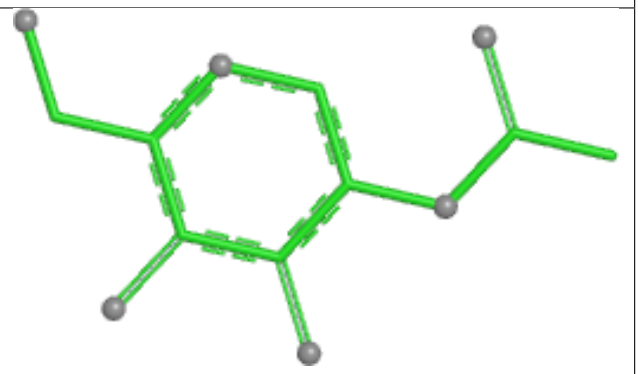
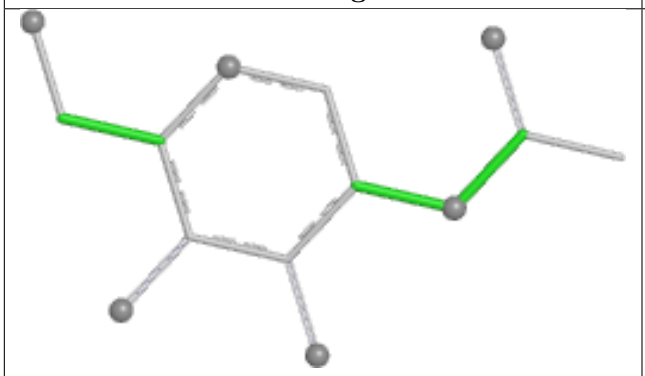


Bond angles



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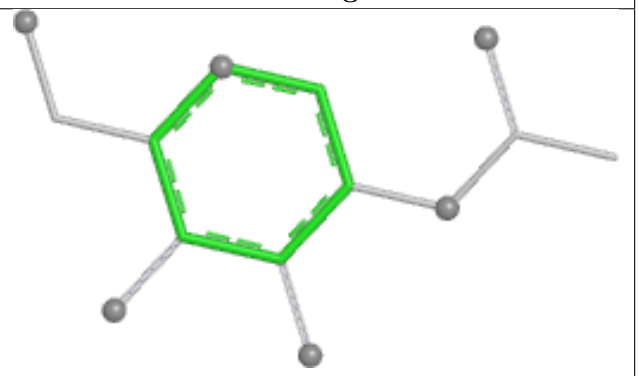
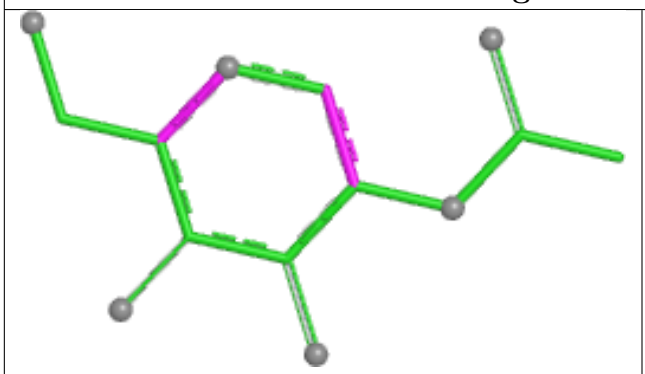


Rings

Ligand NAG B 1305



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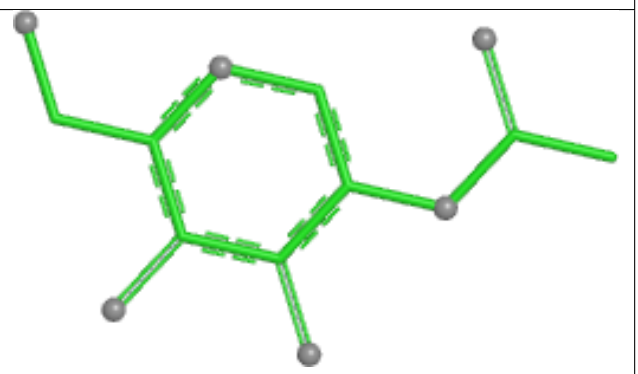
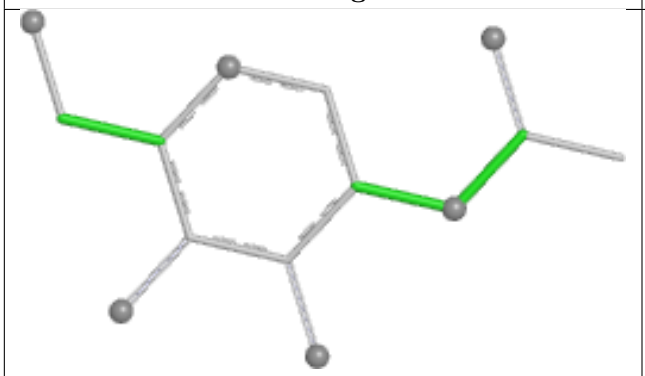


Bond angles



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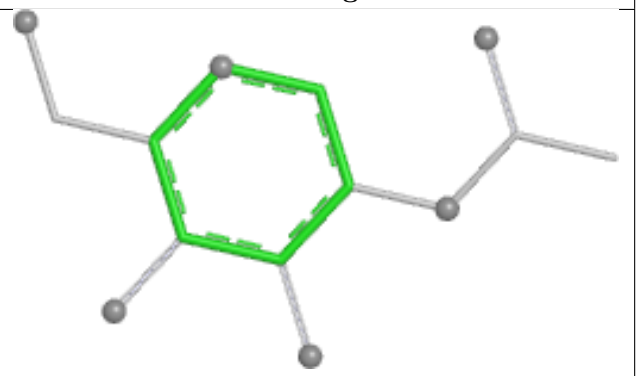
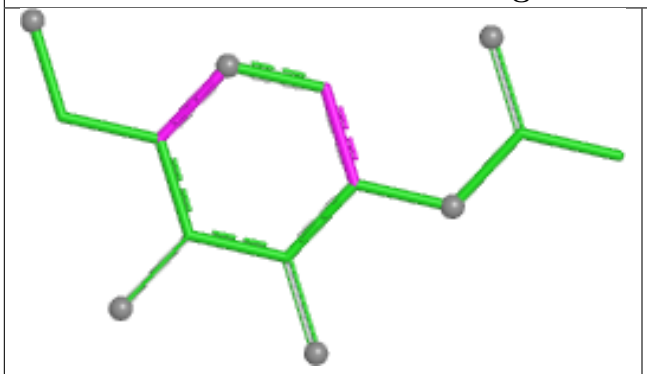


Rings

Ligand NAG B 1311



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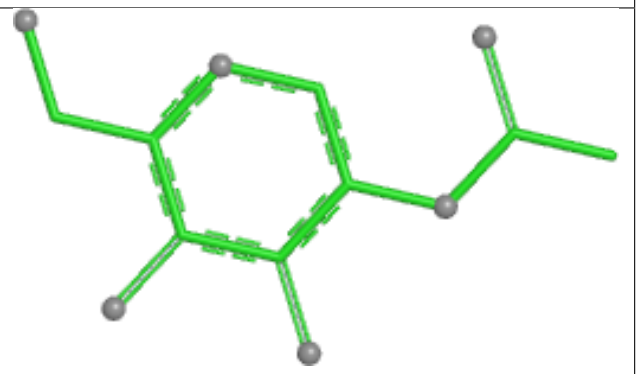
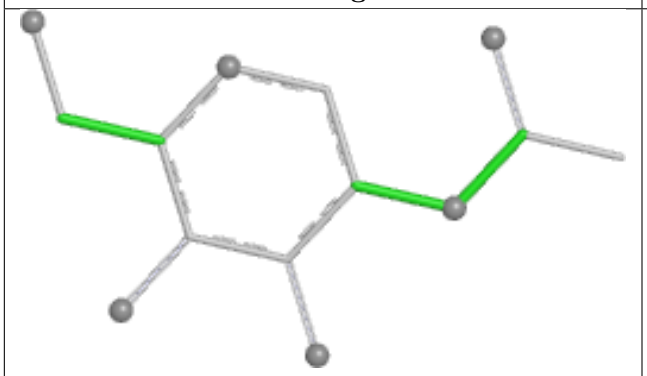


Bond angles



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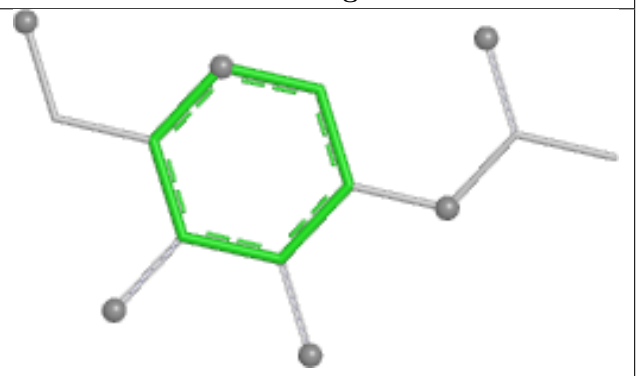
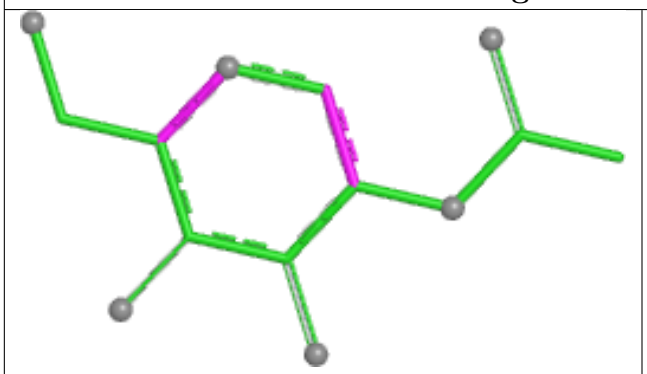


Rings

Ligand NAG A 1310



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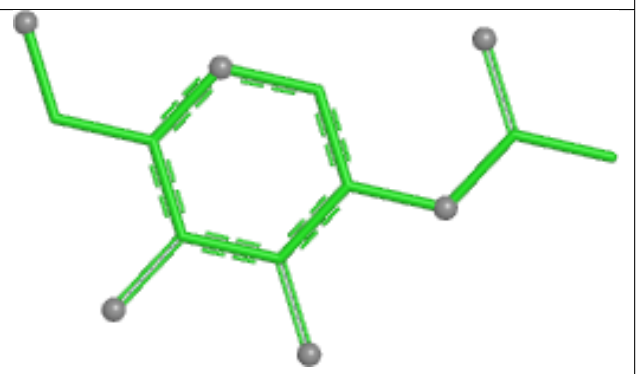

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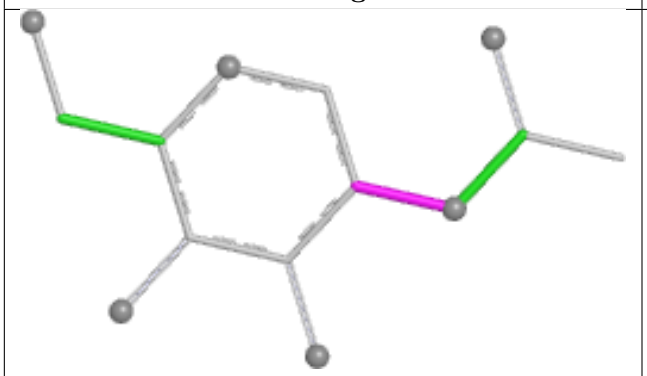

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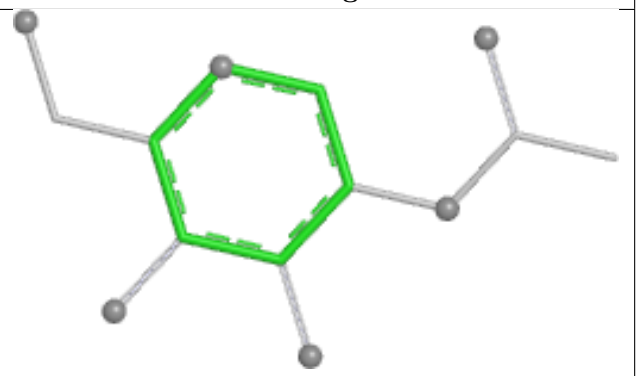
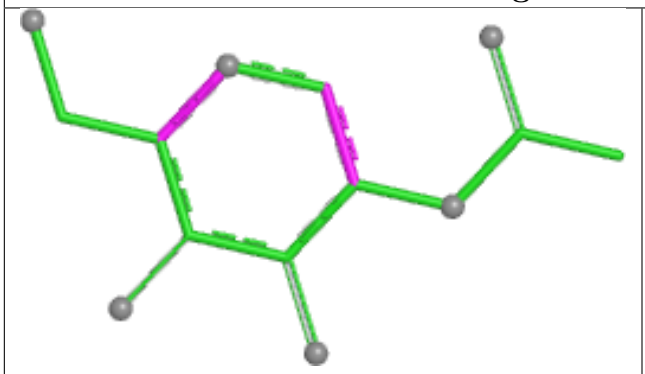


Rings

Ligand NAG C 1312



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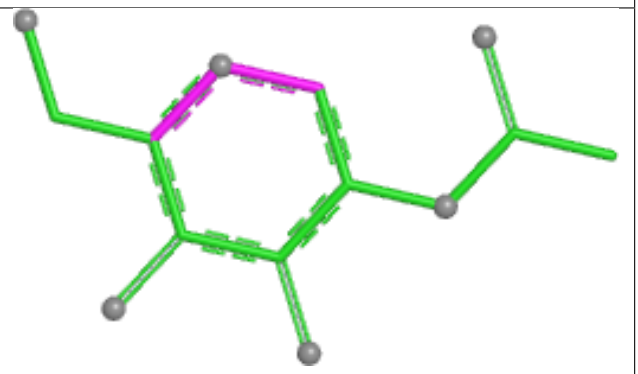
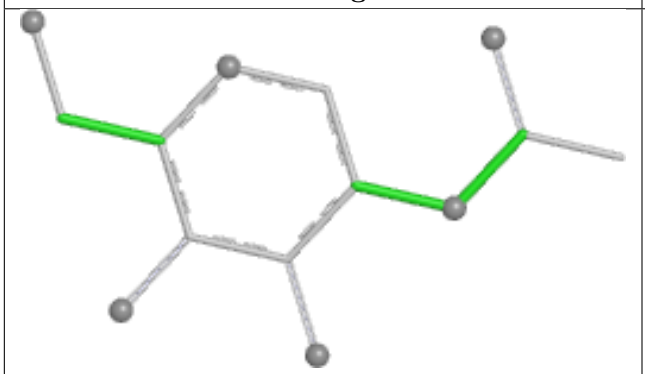


Bond angles



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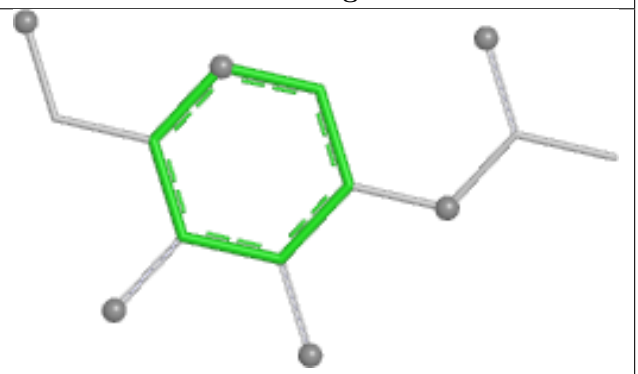
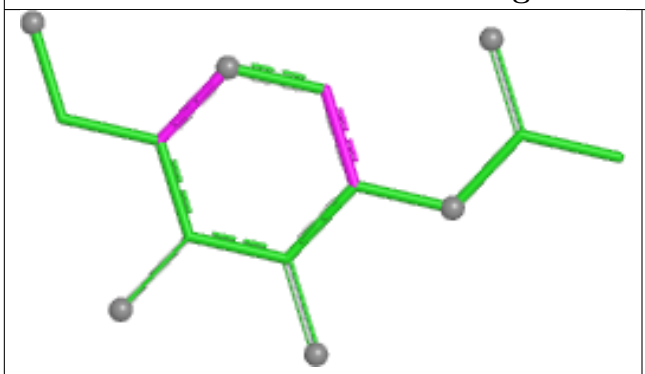


Rings

Ligand NAG B 1310



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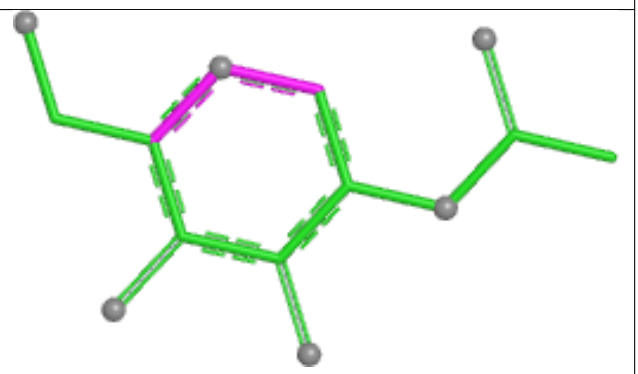
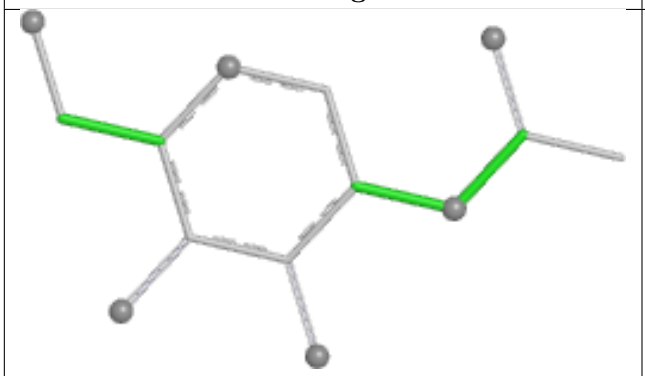


Bond angles



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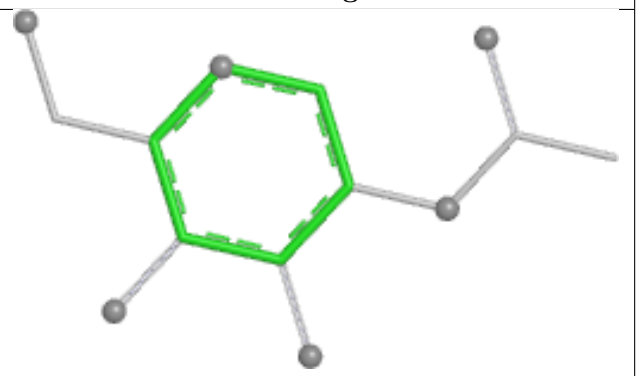
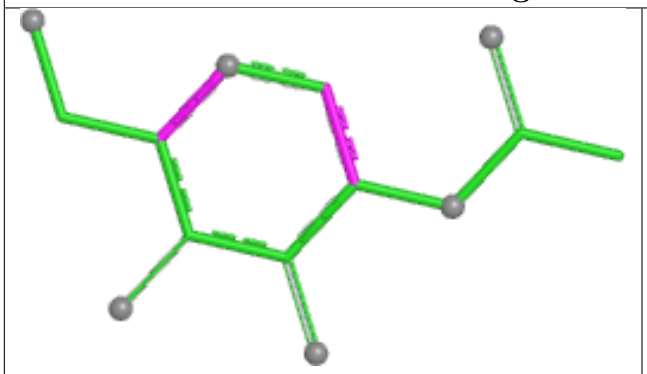


Rings

Ligand NAG C 1313



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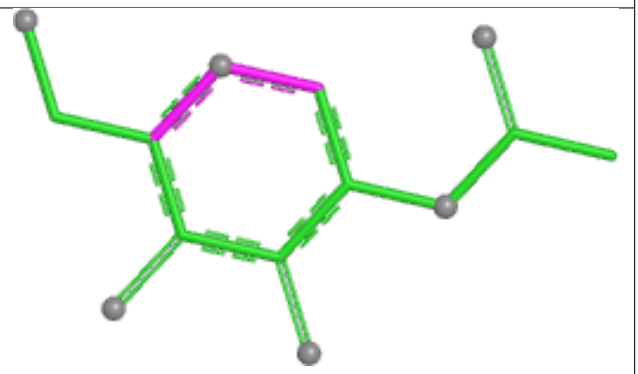

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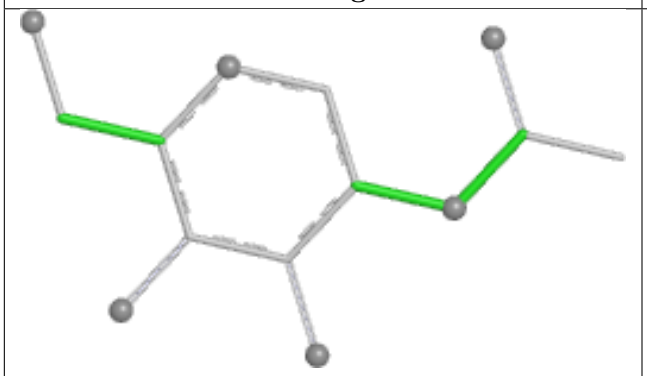

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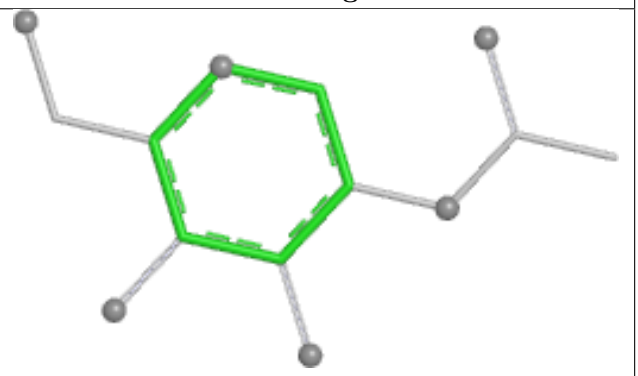
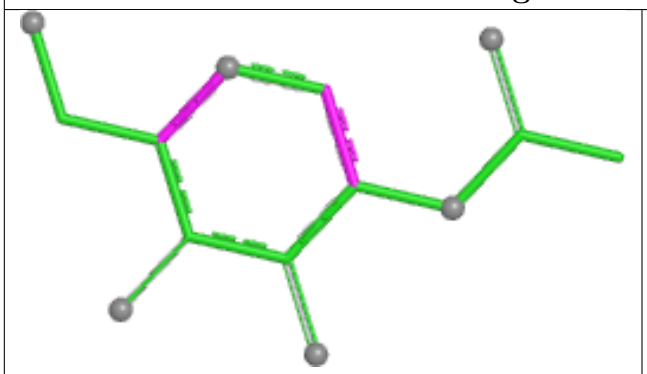


Rings

Ligand NAG B 1307



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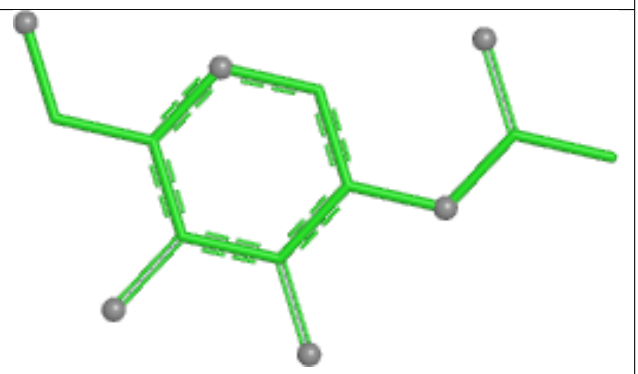
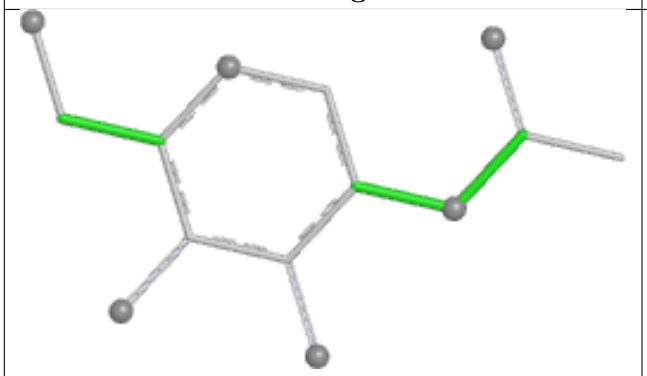


Bond angles



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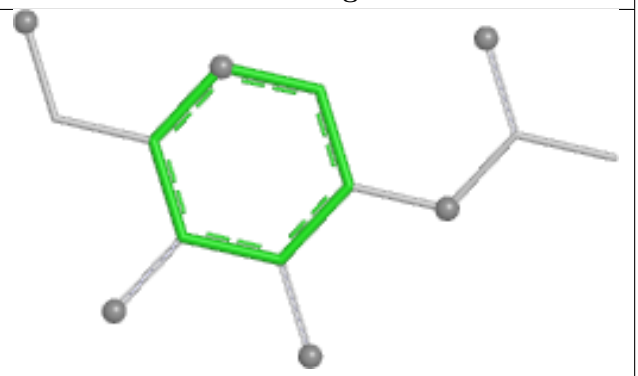
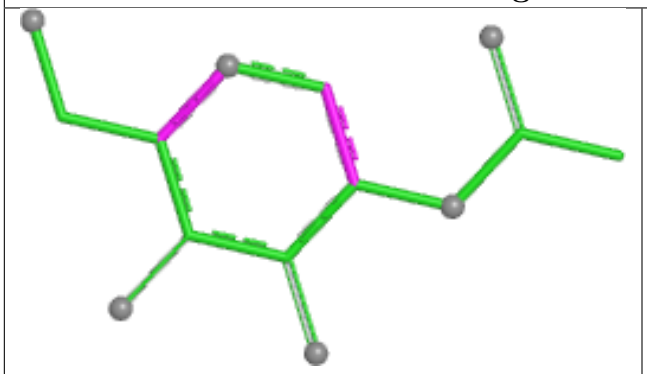


Rings

Ligand NAG C 1303



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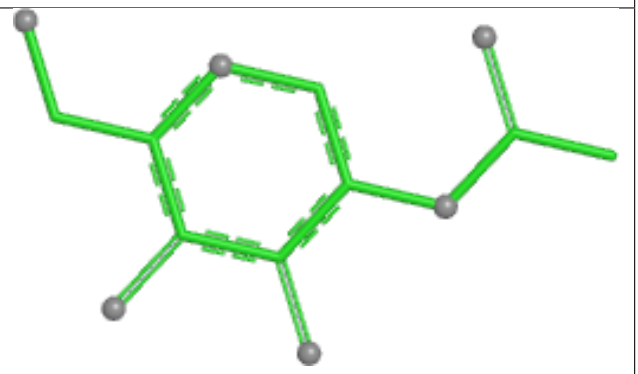
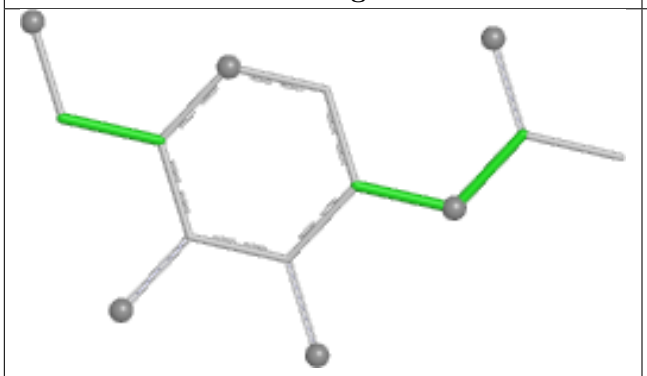


Bond angles



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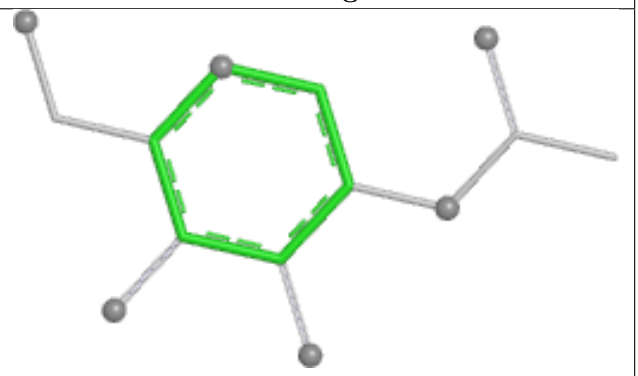
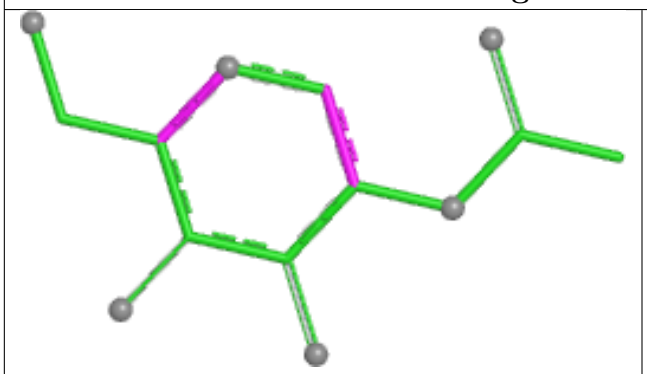


Rings

Ligand NAG A 1308



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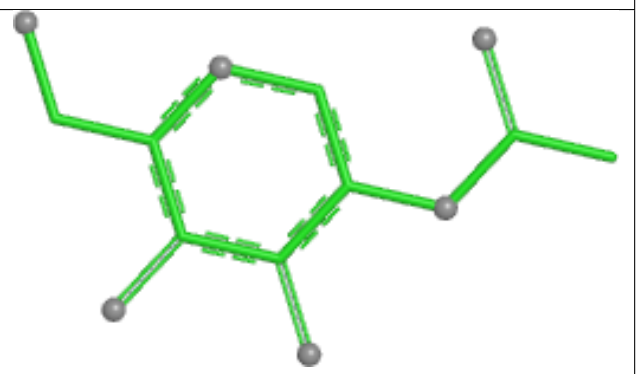
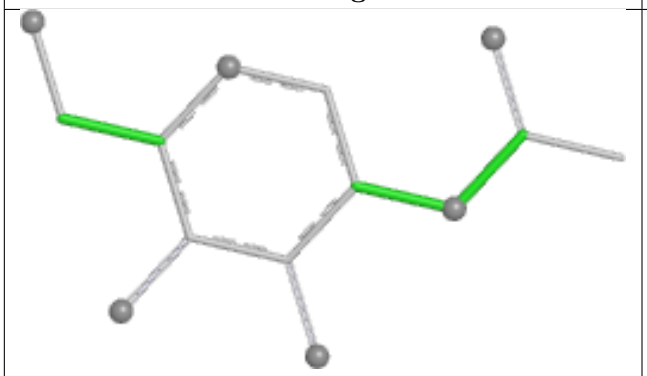


Bond angles



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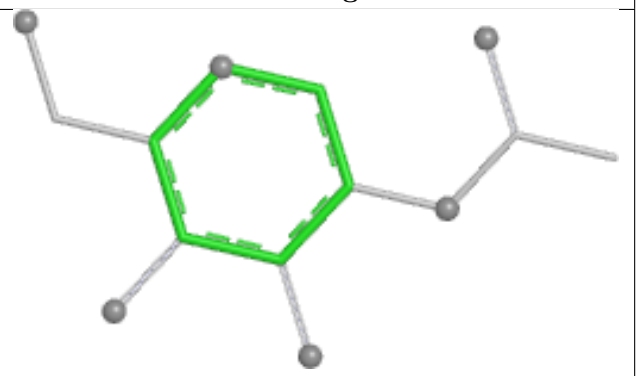
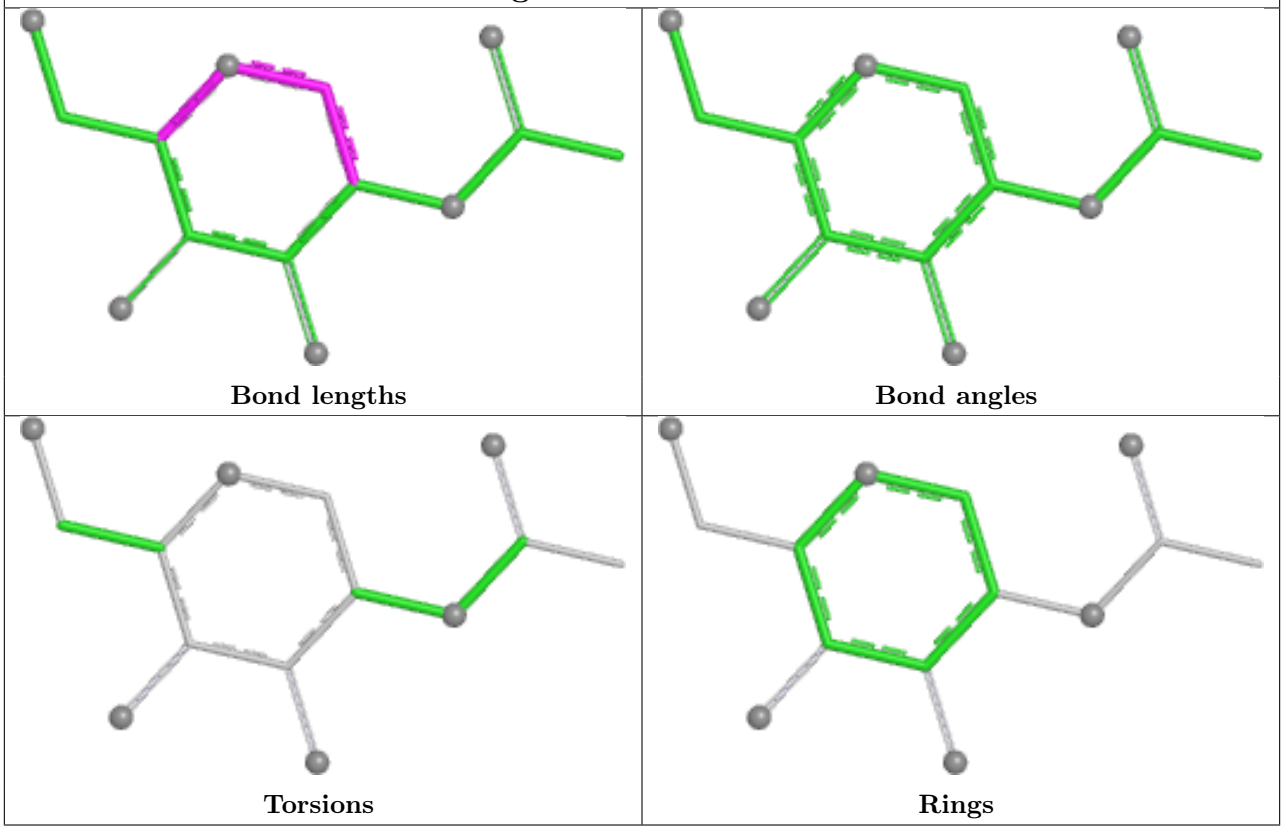
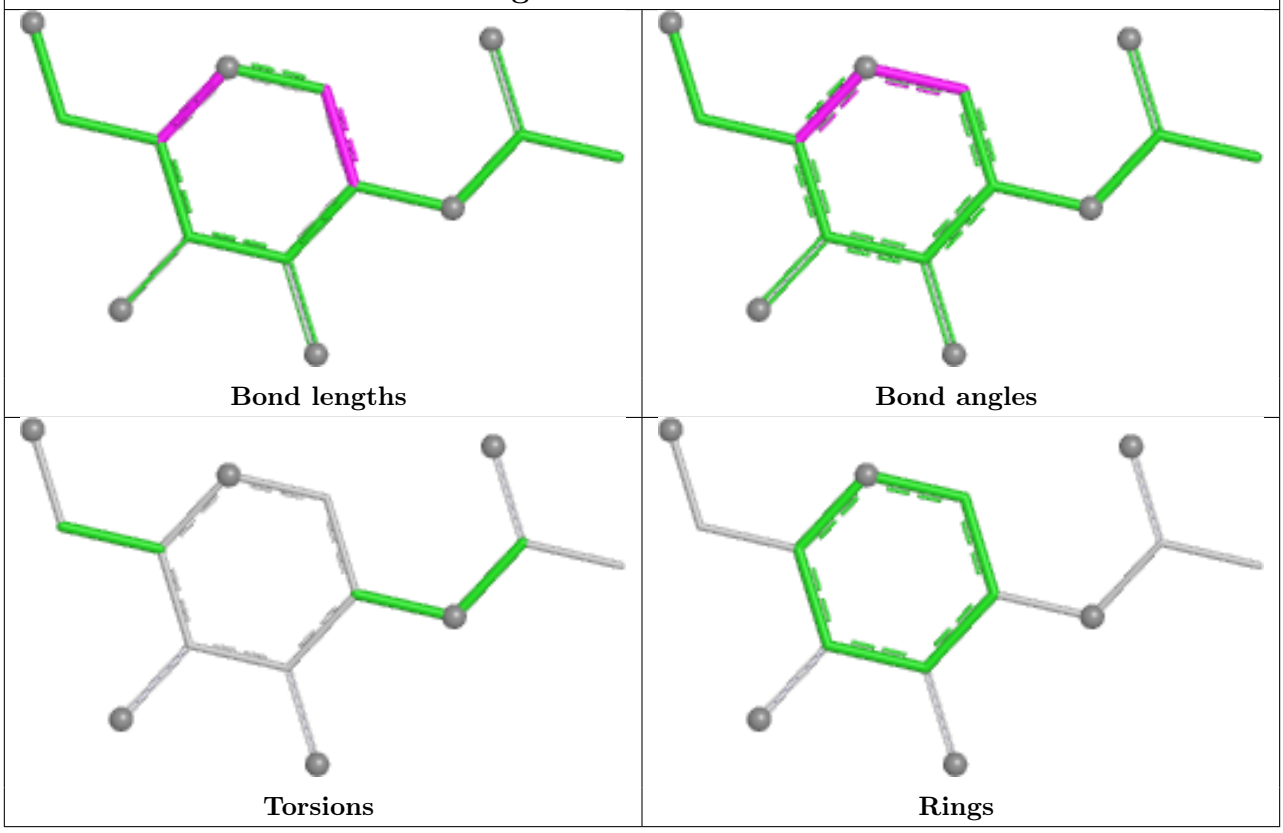


Rings

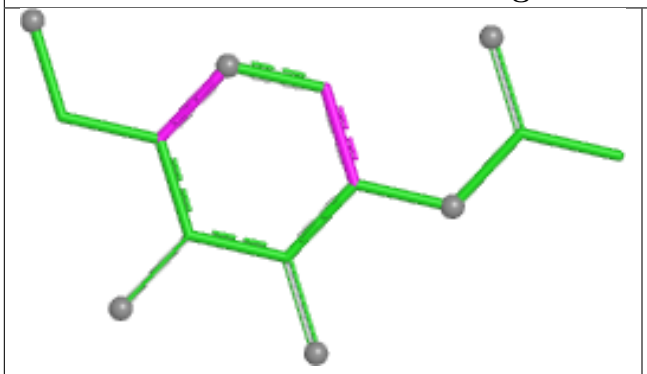
Ligand NAG A 1305



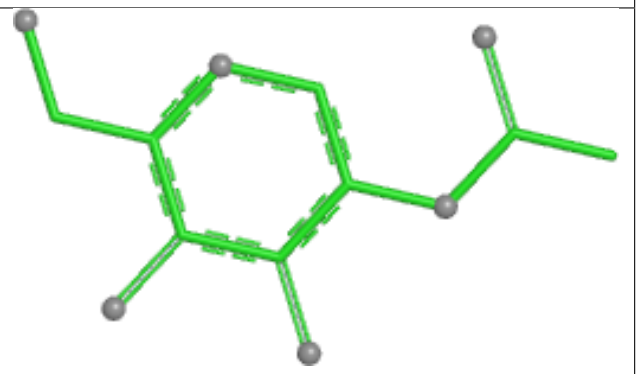
Ligand NAG A 1313



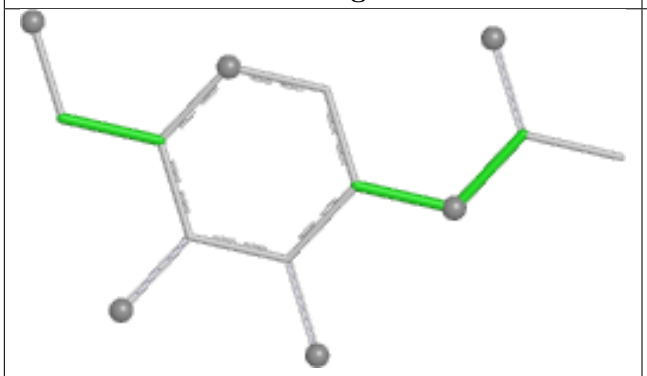
Ligand NAG C 1301



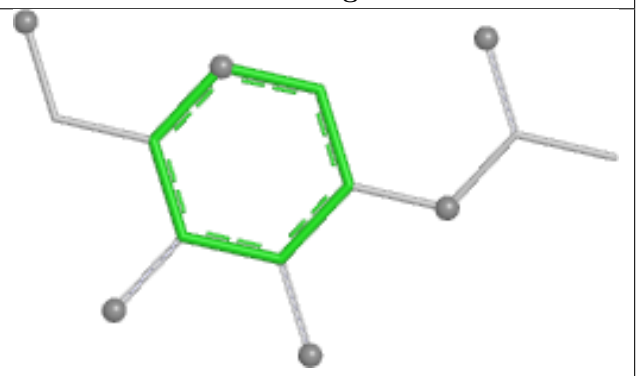
Bond lengths



Bond angles

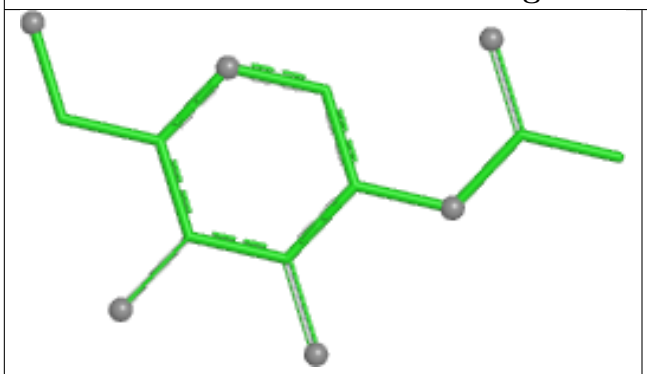


Torsions



Rings

Ligand NAG F 701



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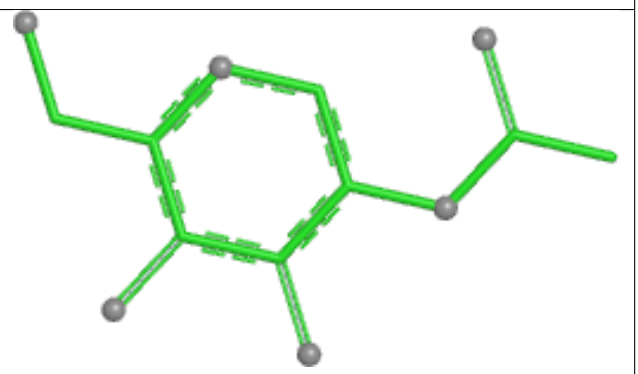
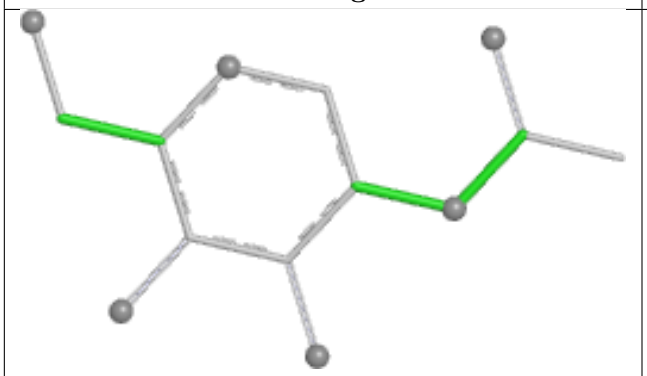


Bond angles



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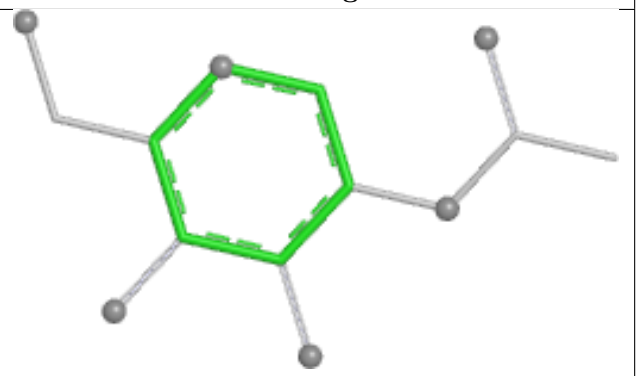
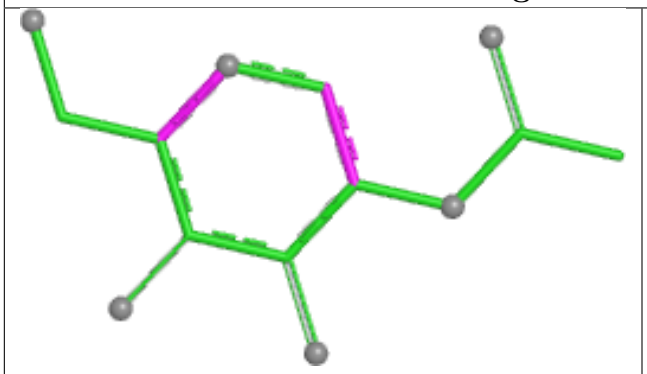


Rings

Ligand NAG B 1308



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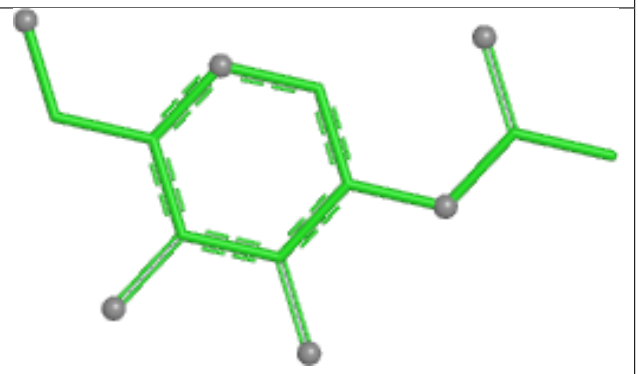
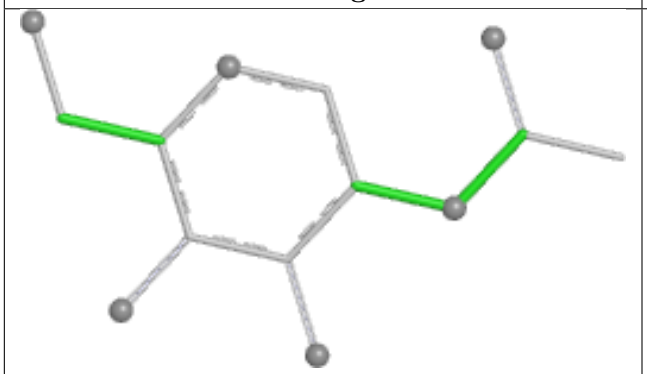


Bond angles



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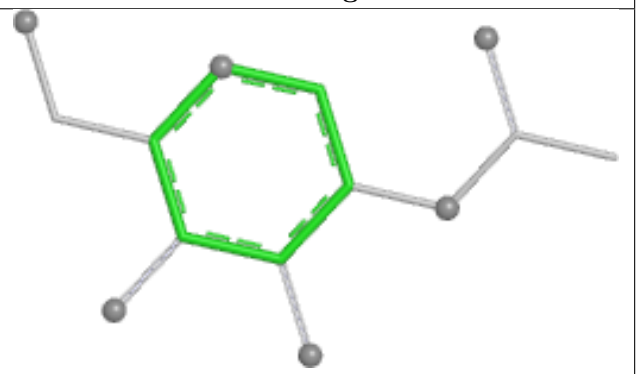
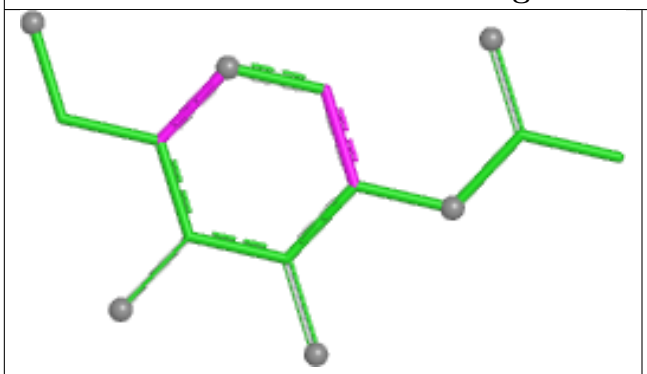


Rings

Ligand NAG B 1312



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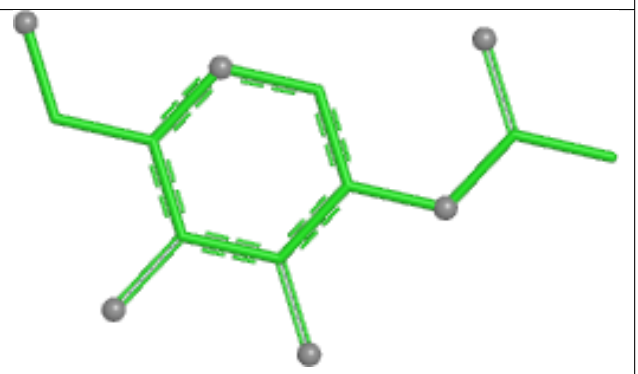
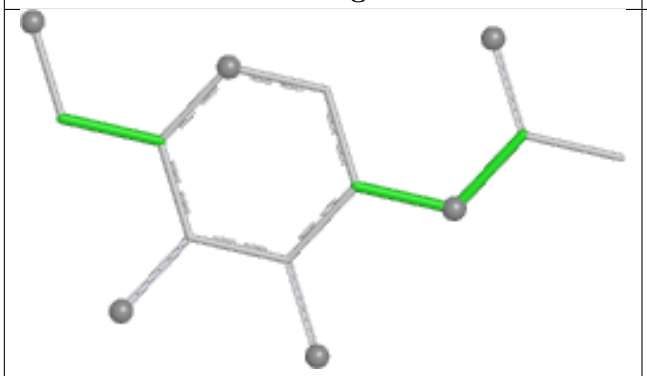
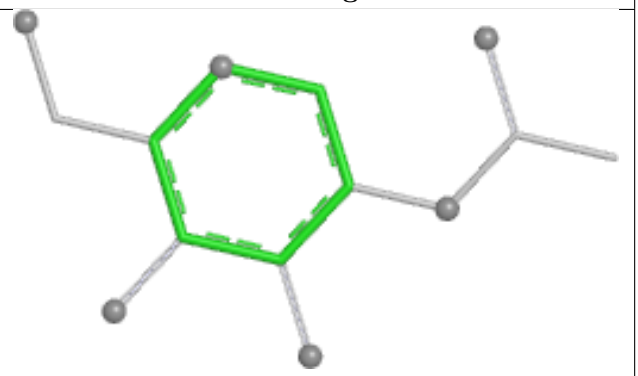


Bond angles

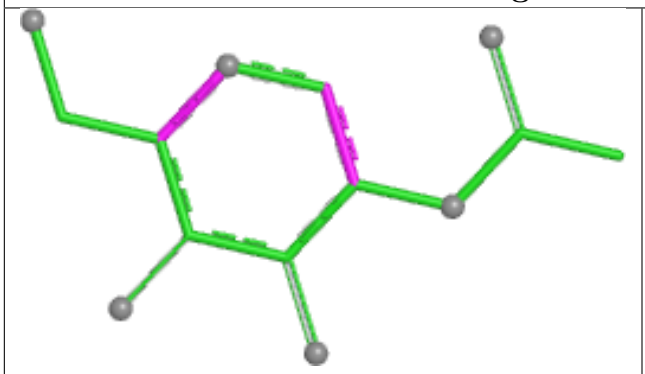


Torsions



Rings

Ligand NAG A 1303



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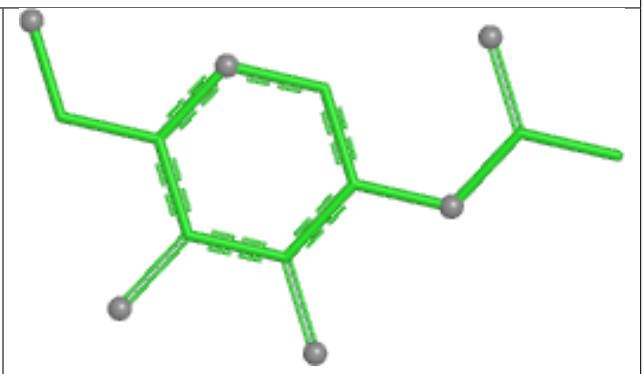
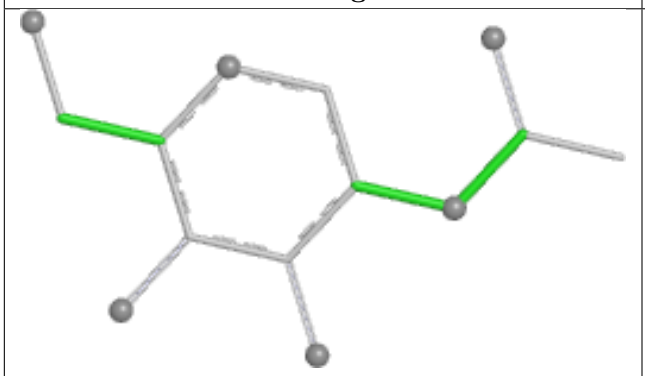


Bond angles



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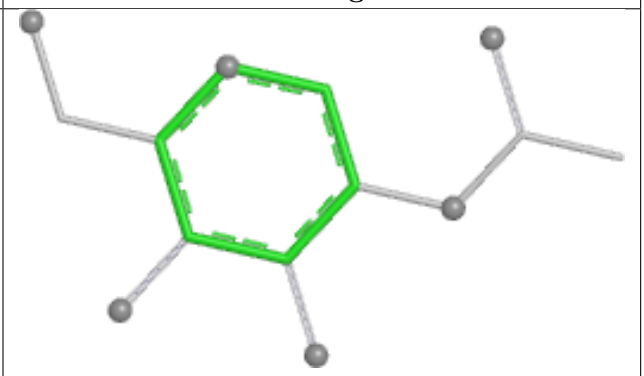
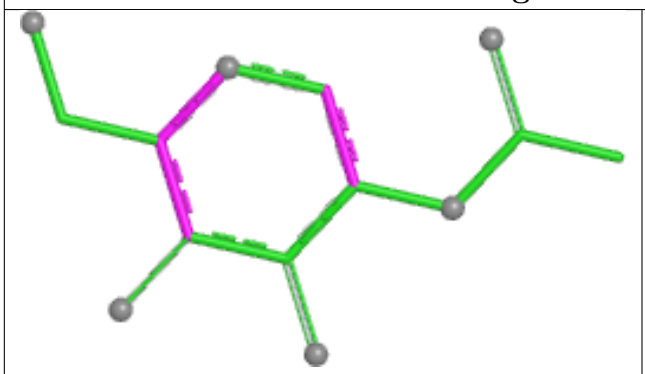


Rings

Ligand NAG C 1306



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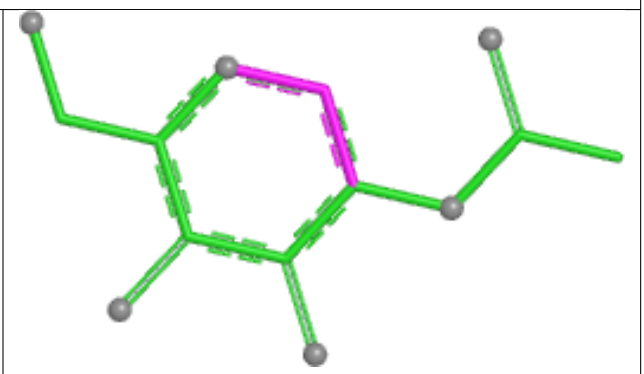
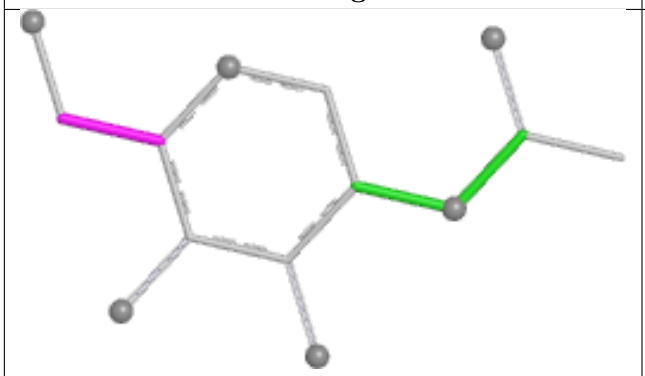


Bond angles



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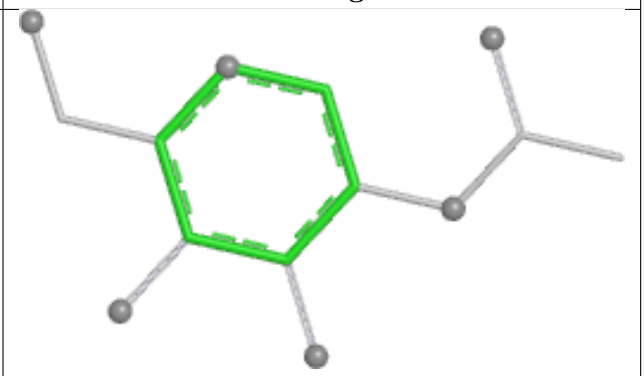
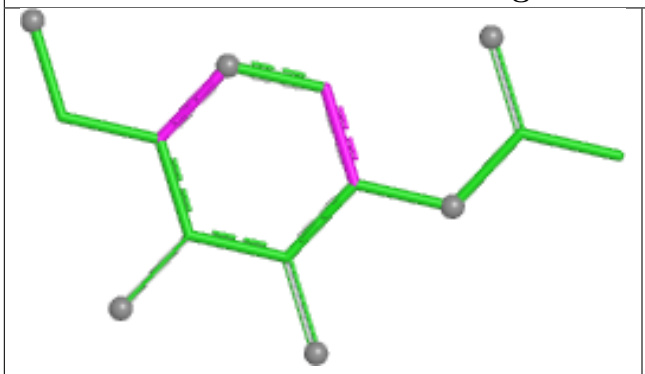


Rings

Ligand NAG C 1309



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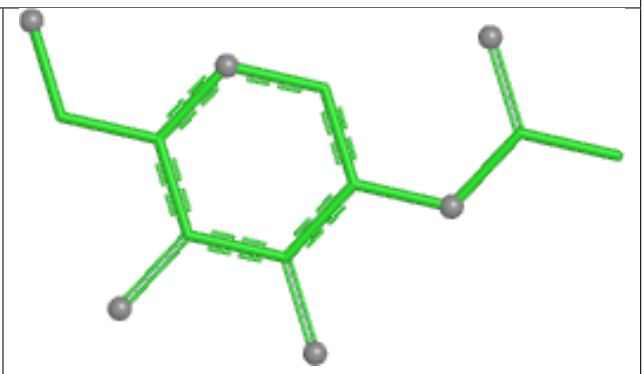
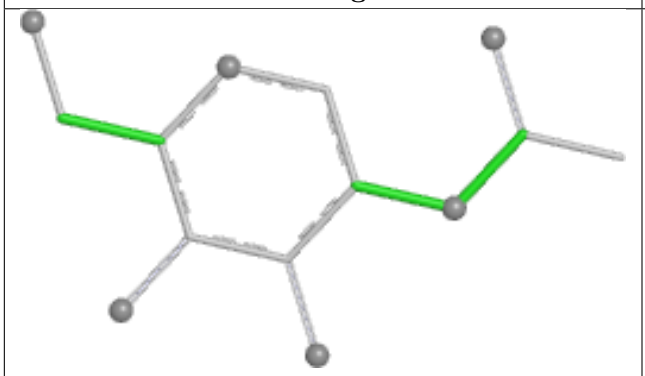


Bond angles



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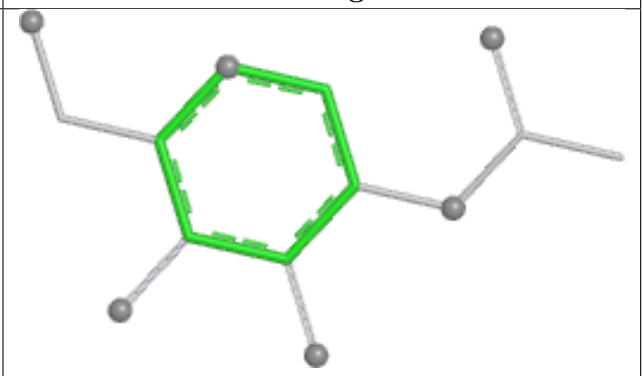
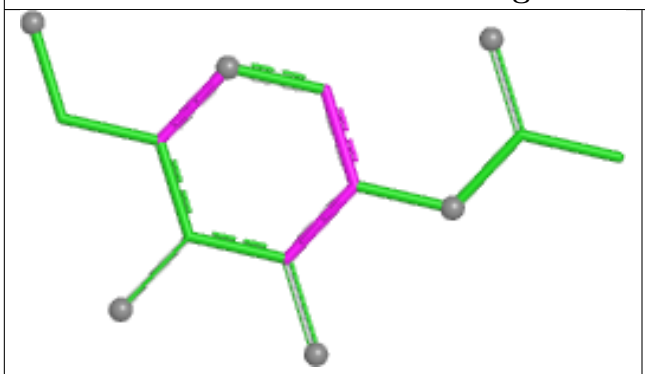


Rings

Ligand NAG B 1313



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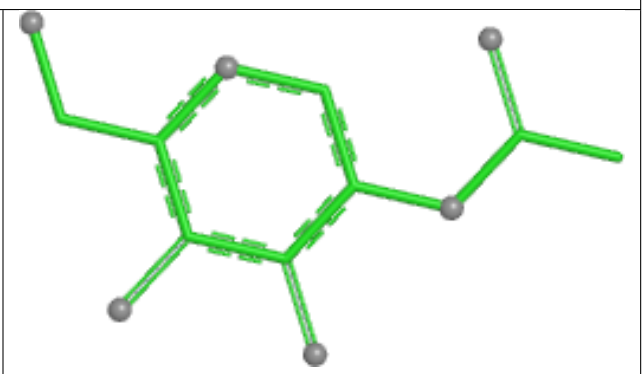
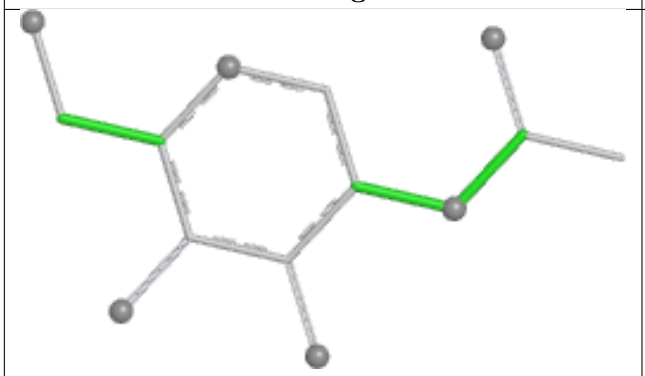
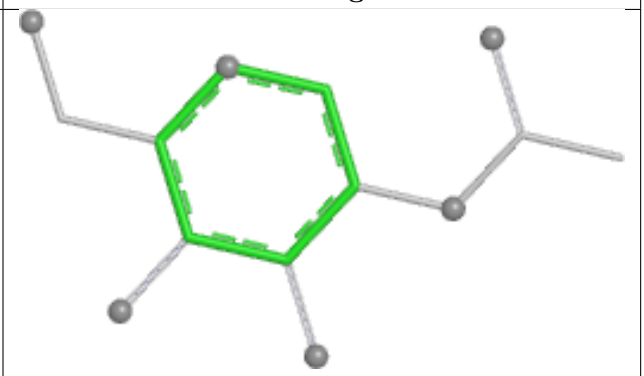


Bond angles

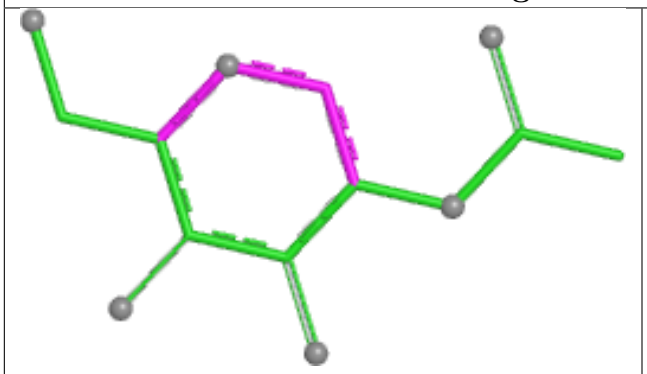


Torsions



Rings

Ligand NAG C 1304



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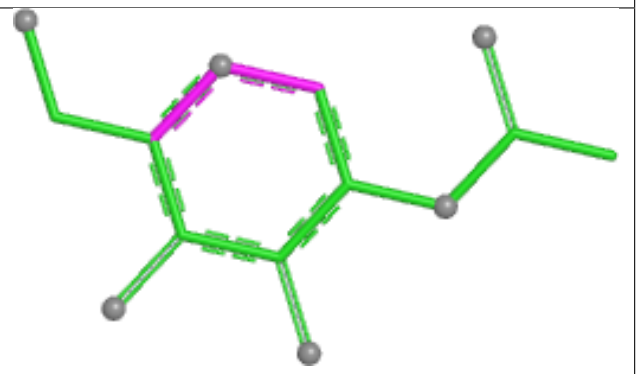
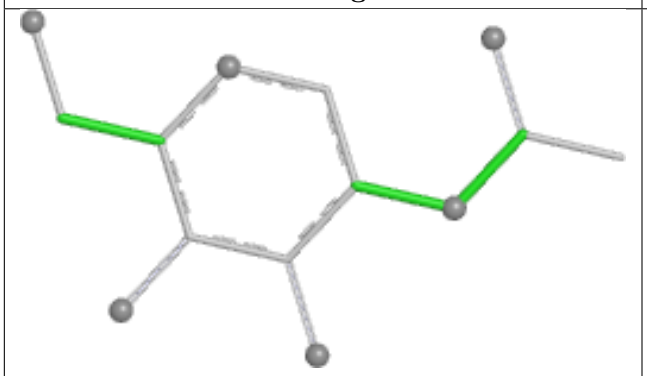


Bond angles



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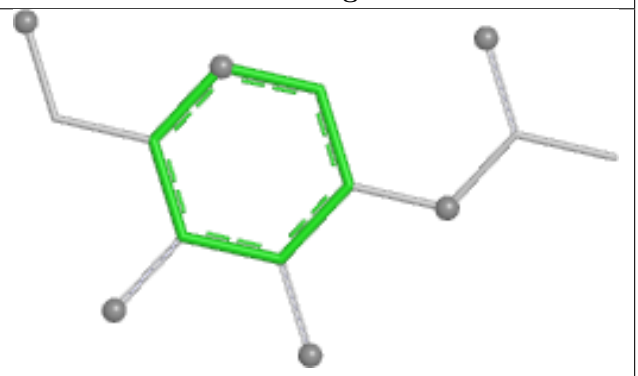
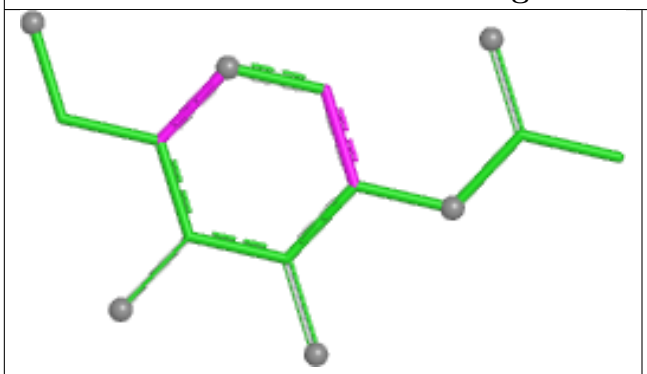


Rings

Ligand NAG A 1312



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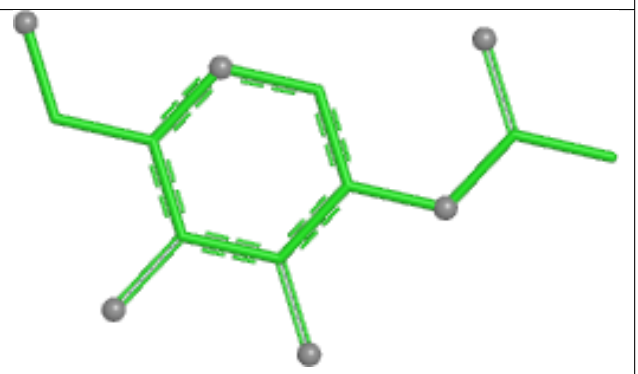
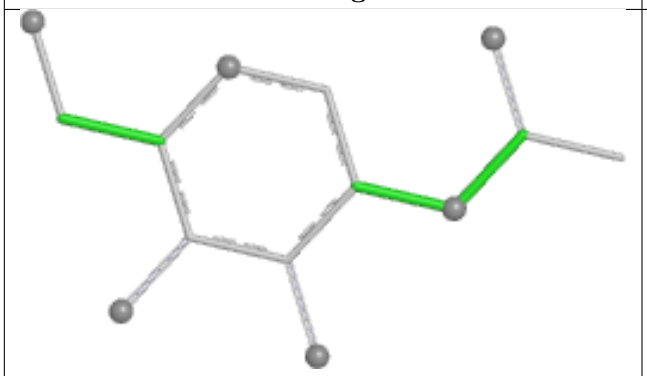


Bond angles



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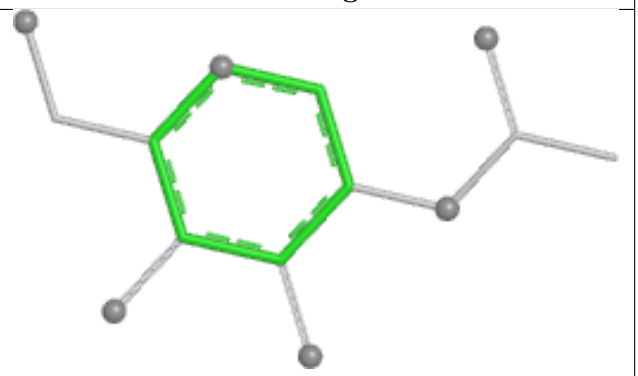
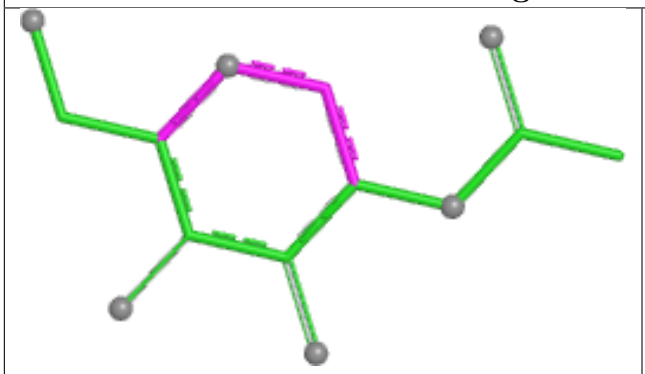


Rings

Ligand NAG C 1310



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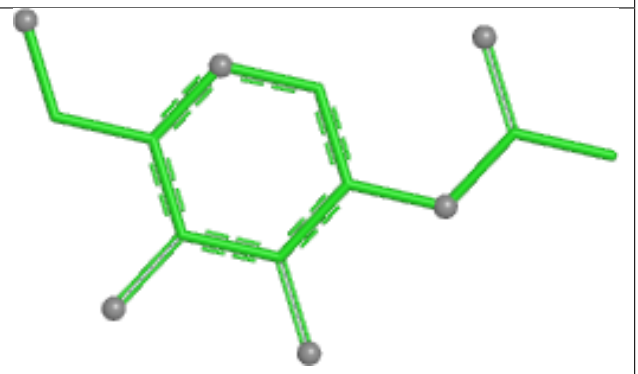
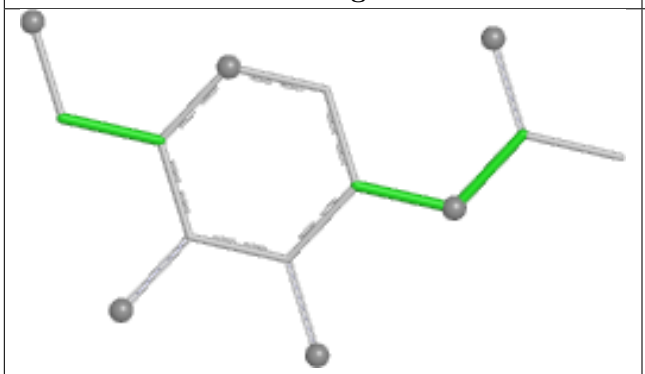


Bond angles



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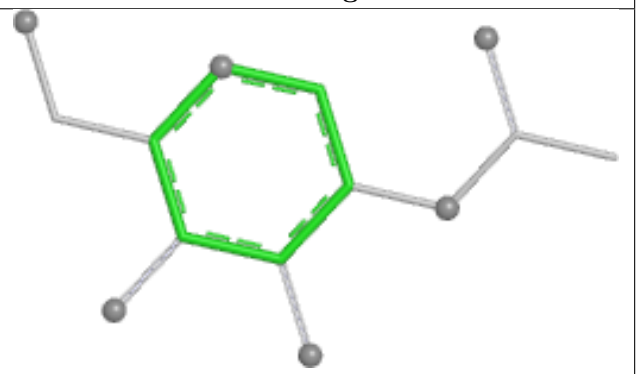
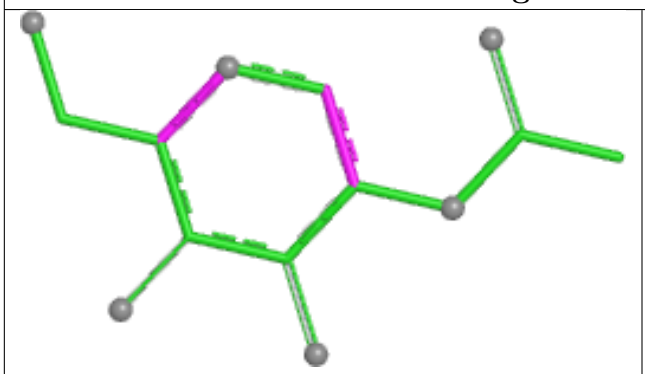


Rings

Ligand NAG C 1311



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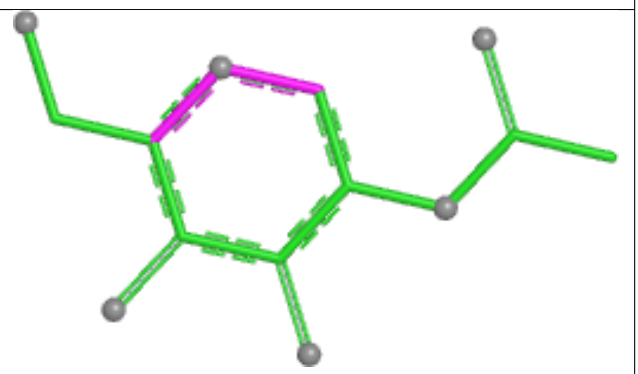
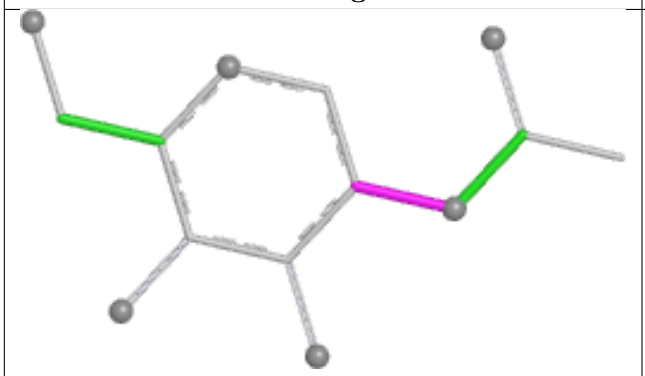


Bond angles



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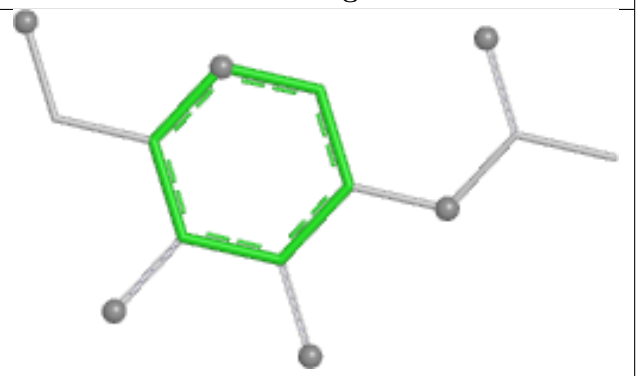
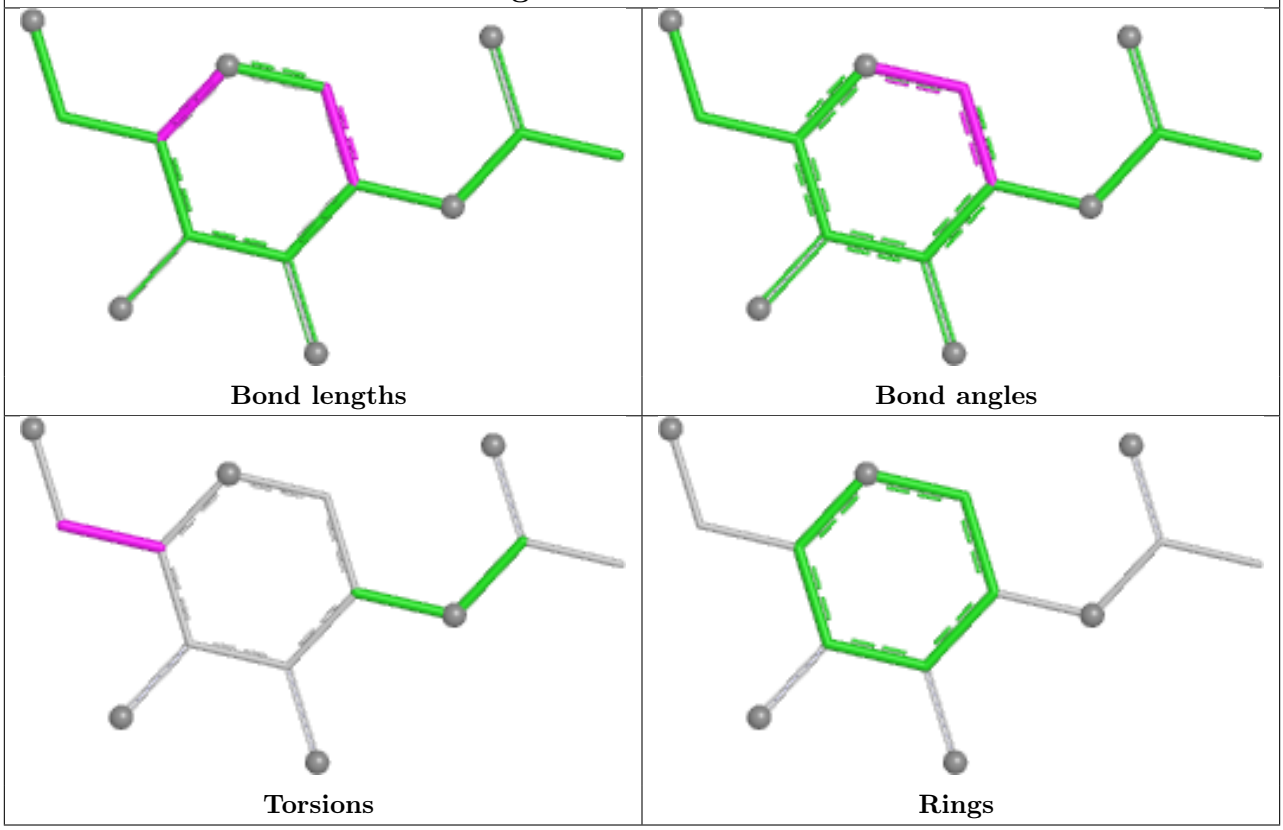
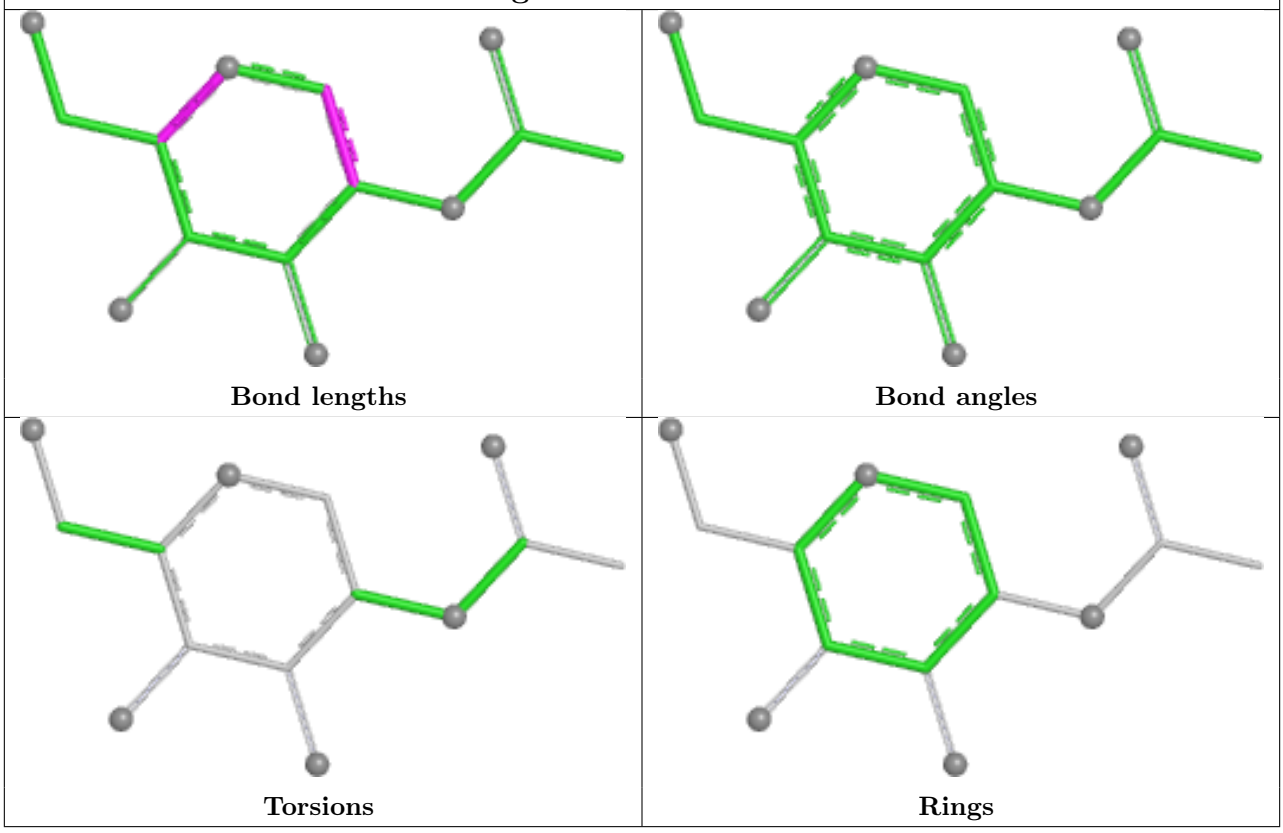


Rings

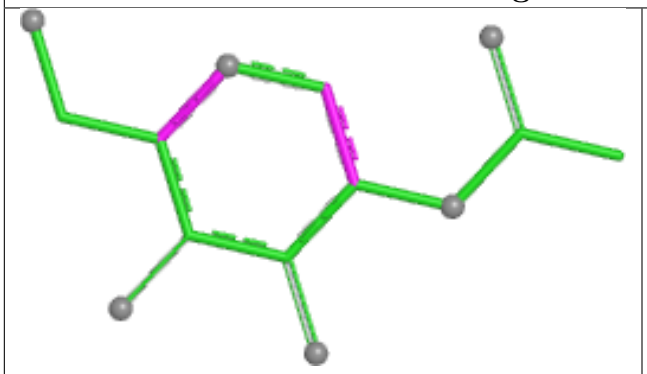
Ligand NAG A 1306



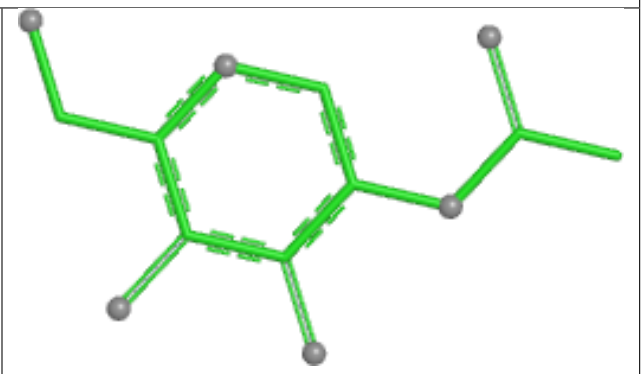
Ligand NAG A 1304



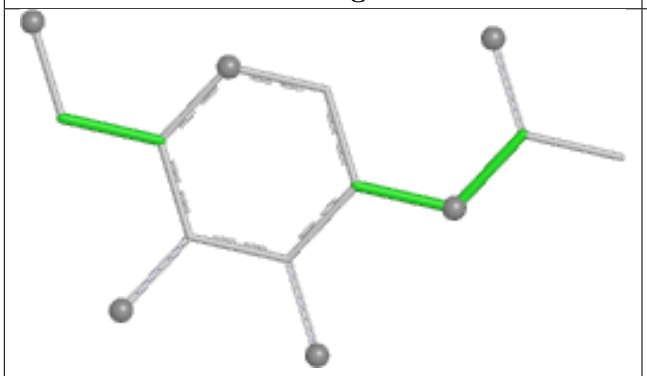
Ligand NAG C 1307



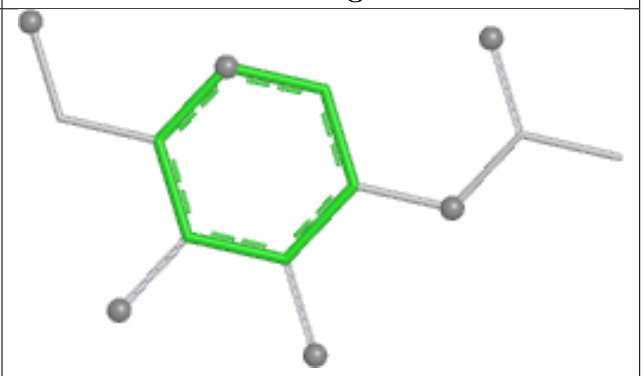
Bond lengths



Bond angles

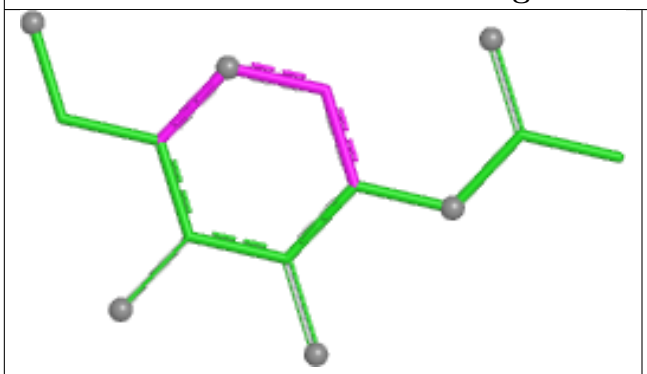


Torsions

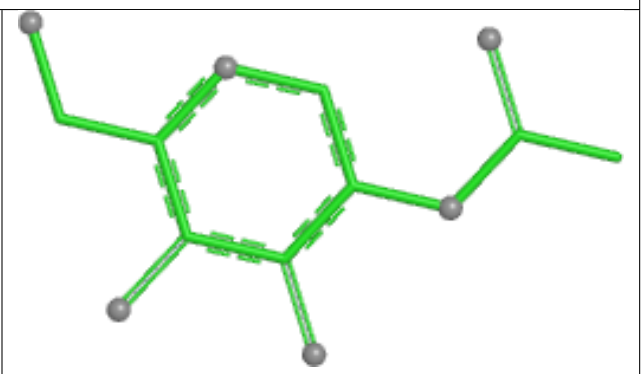


Rings

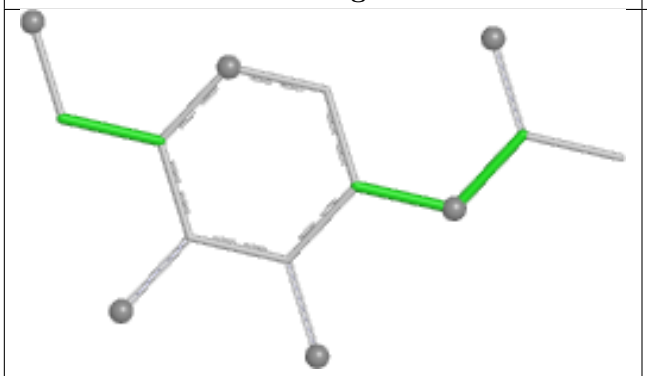
Ligand NAG B 1302



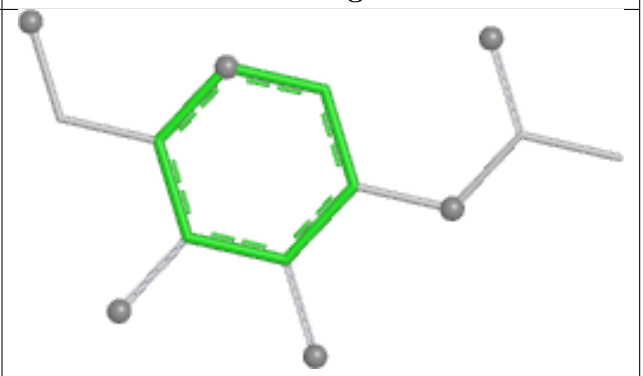
Bond lengths



Bond angles

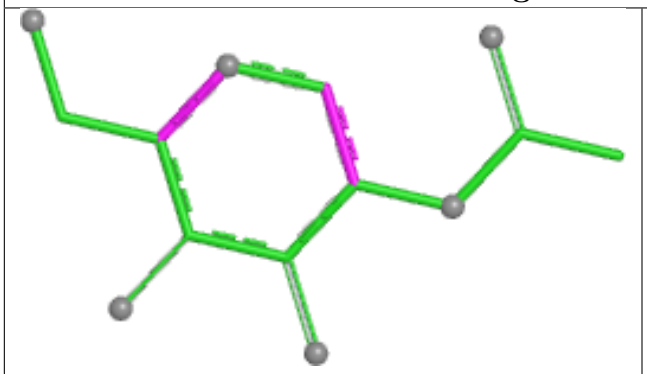


Torsions

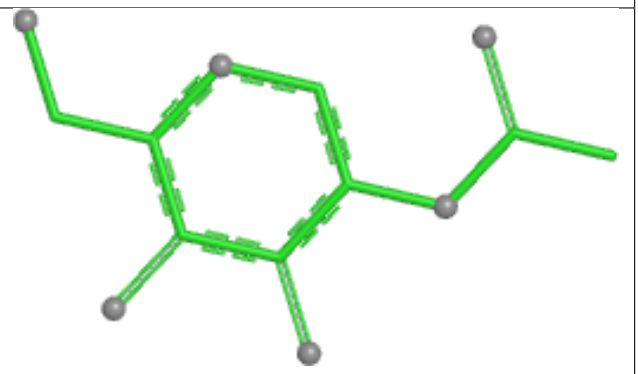


Rings

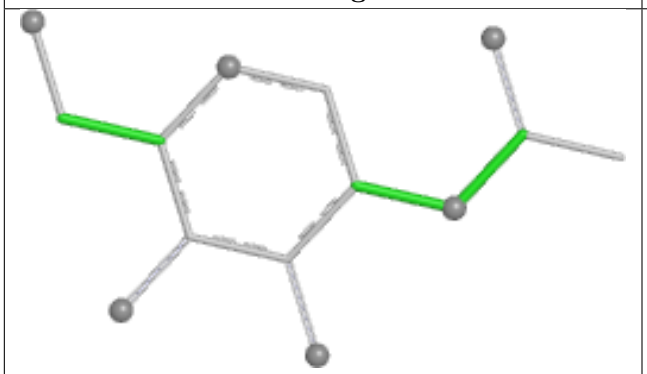
Ligand NAG B 1303



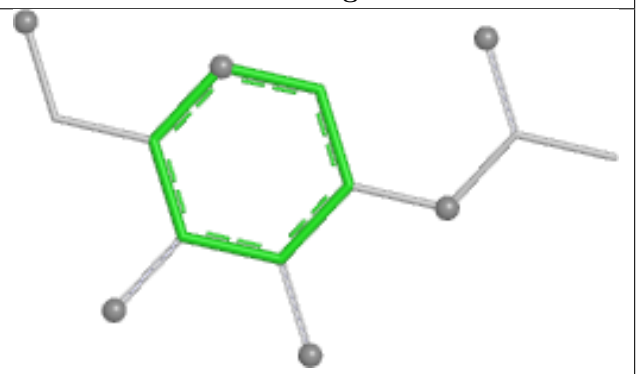
Bond lengths



Bond angles

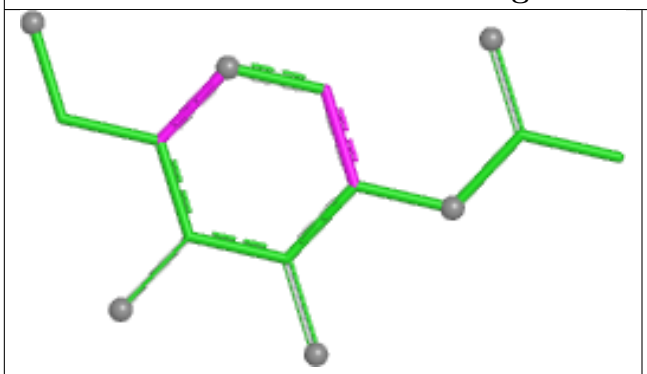


Torsions

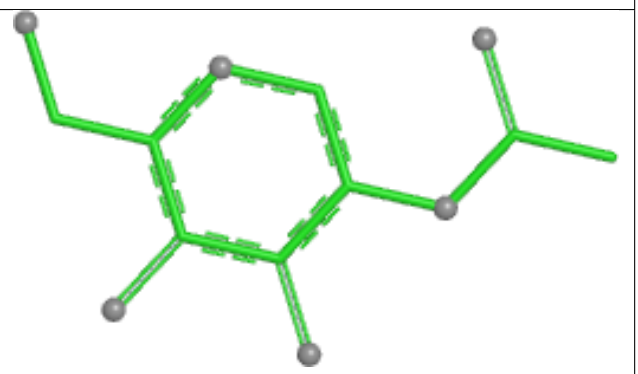


Rings

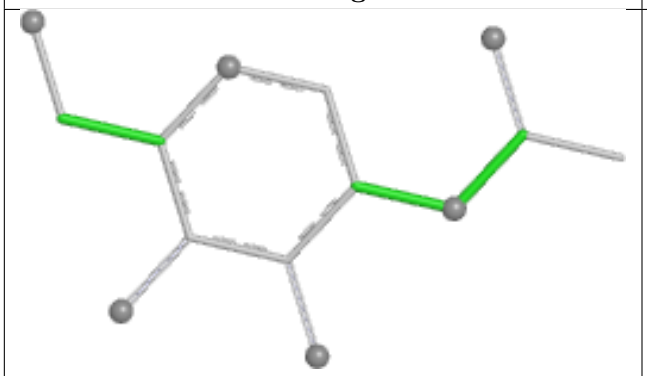
Ligand NAG A 1307



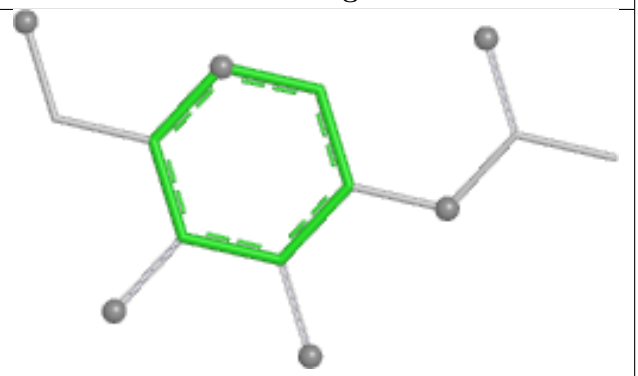
Bond lengths



Bond angles

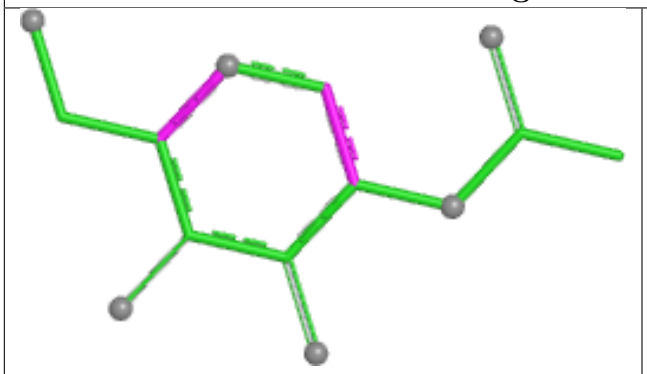


Torsions

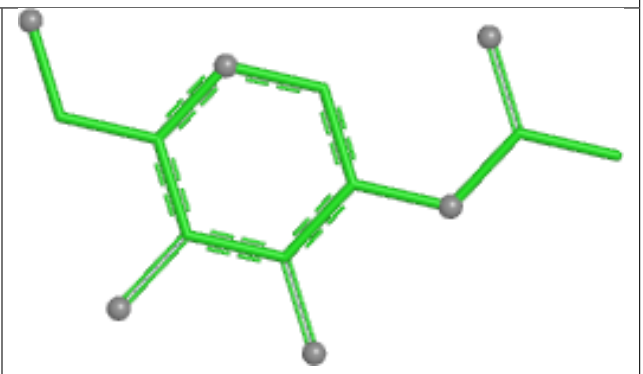


Rings

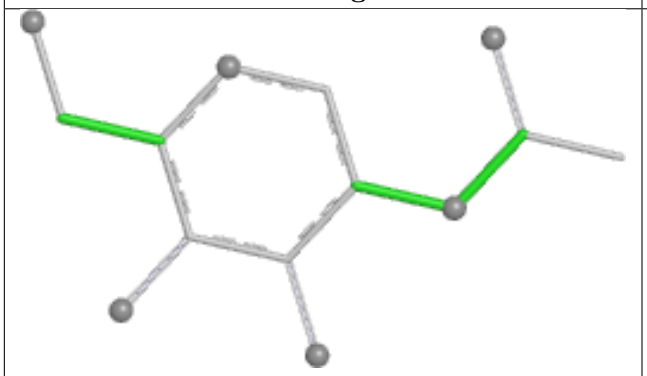
Ligand NAG C 1305



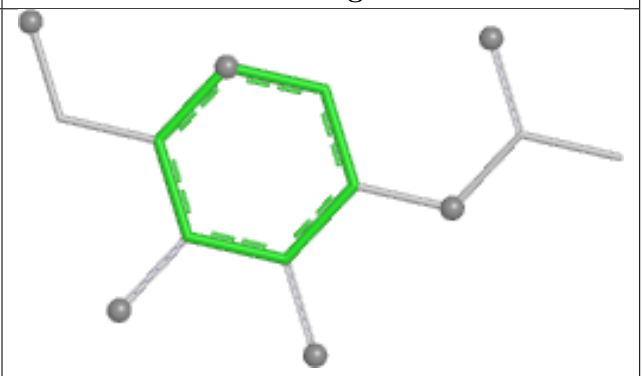
Bond lengths



Bond angles

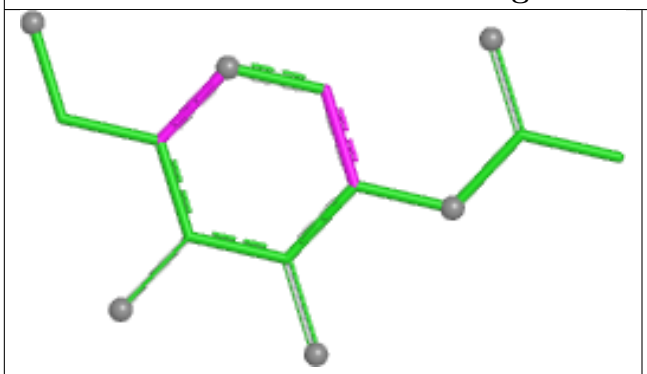


Torsions

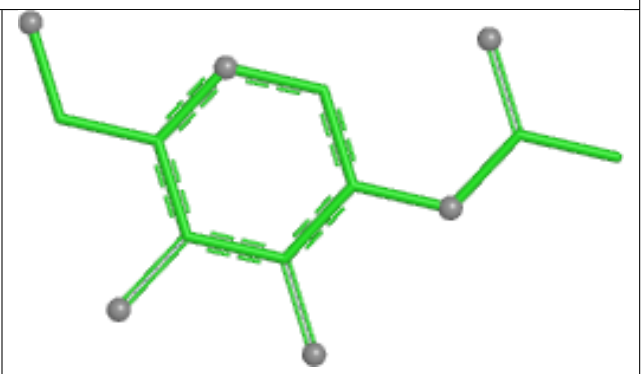


Rings

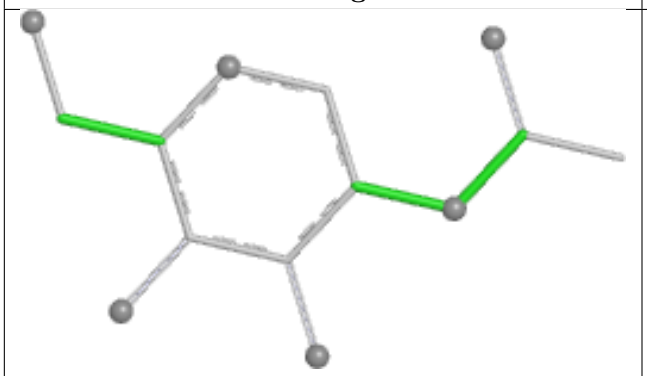
Ligand NAG A 1311



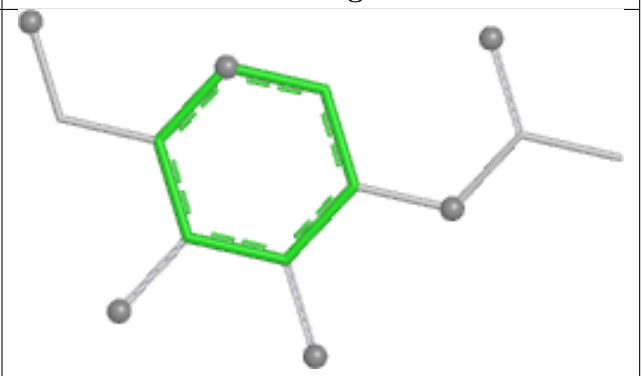
Bond lengths



Bond angles

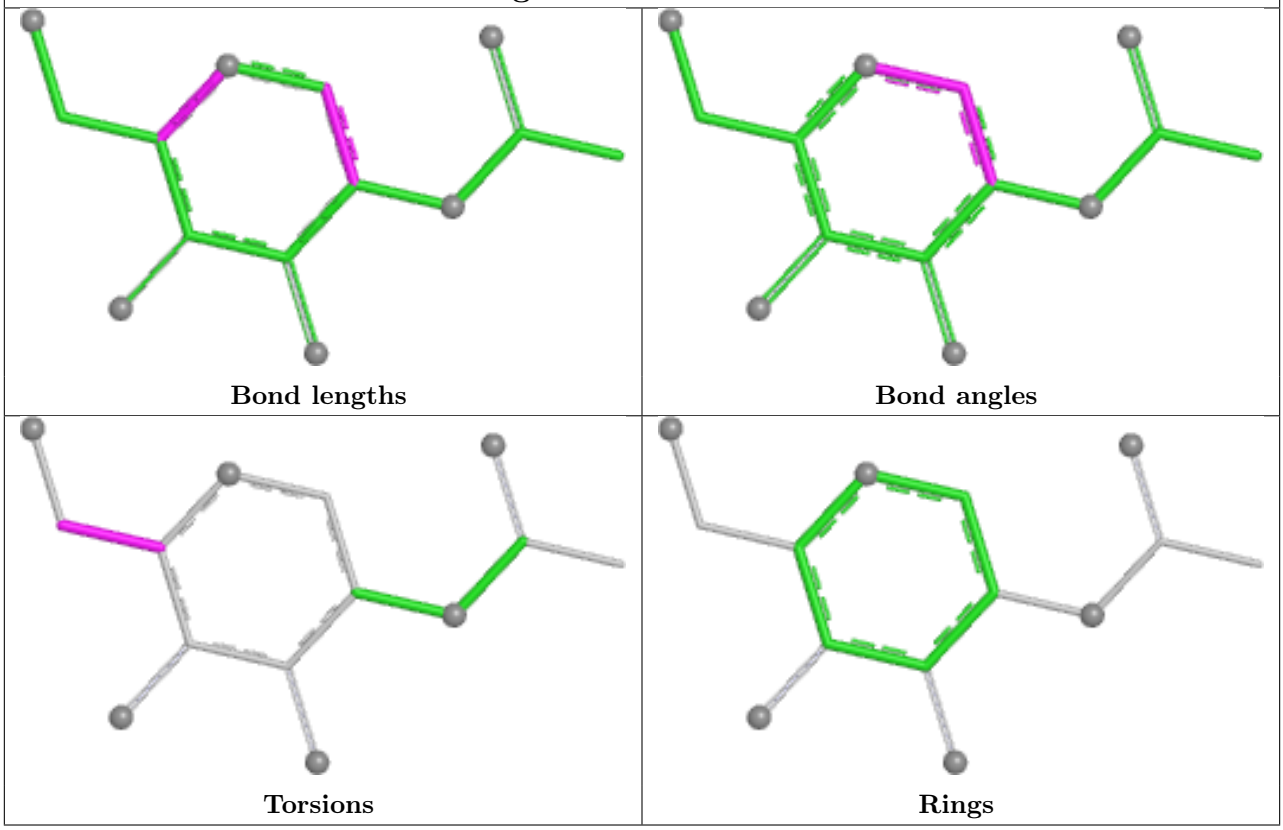


Torsions

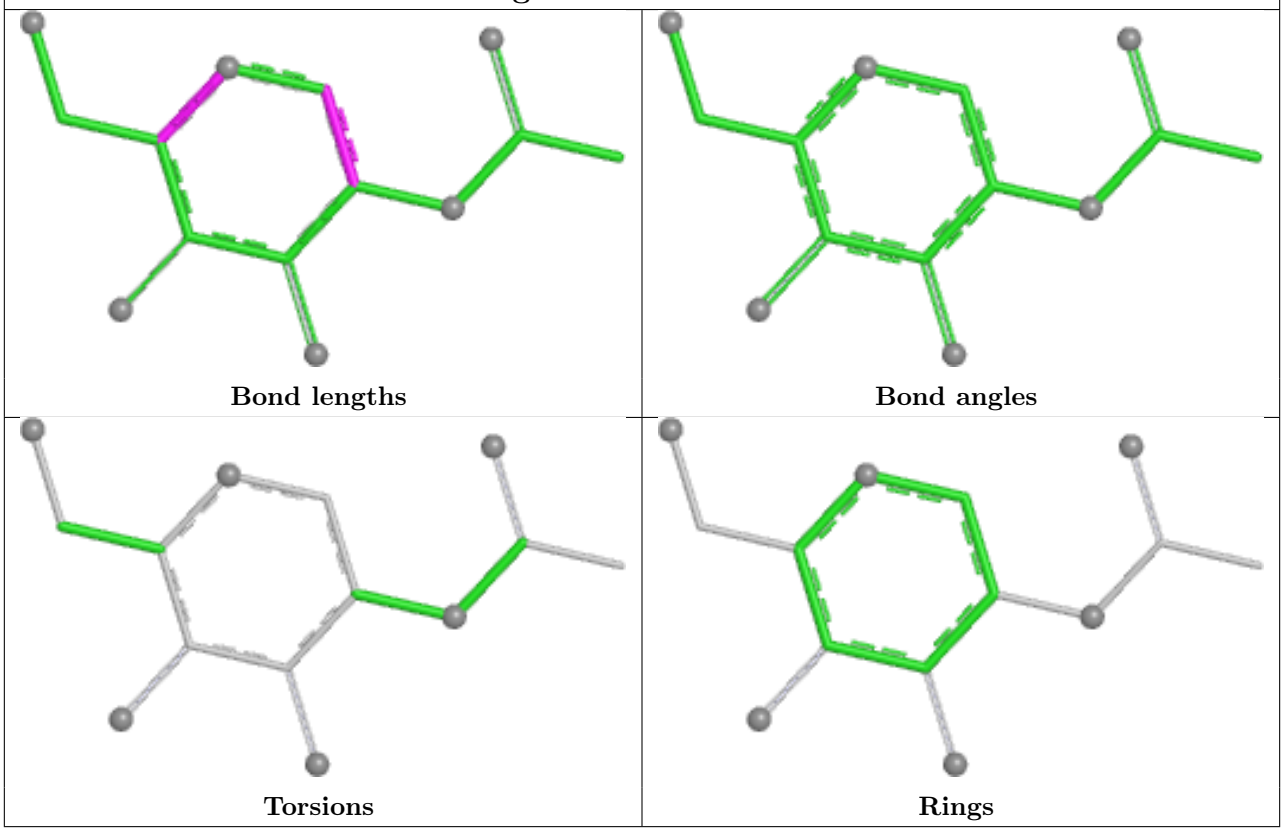


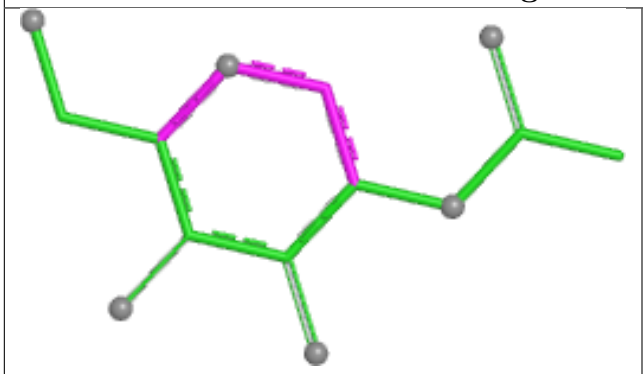
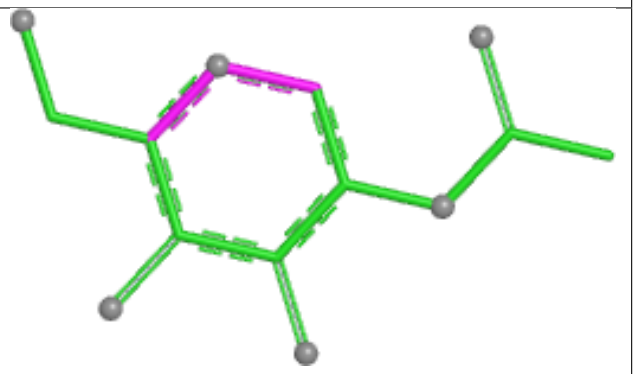
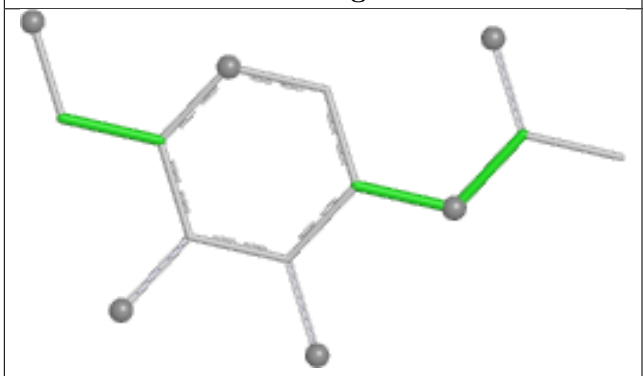
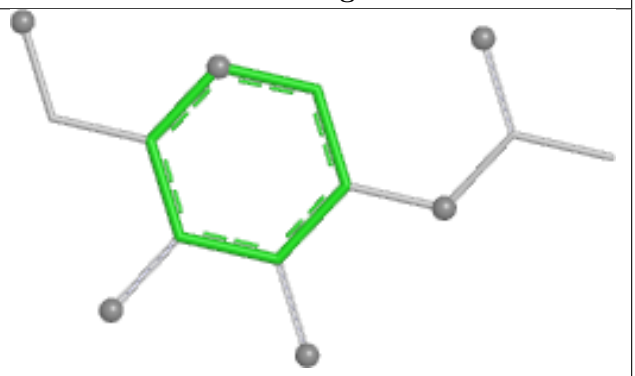
Rings

Ligand NAG B 1306



Ligand NAG B 1301



Ligand NAG D 701	
 Bond lengths	 Bond angles
 Torsions	 Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

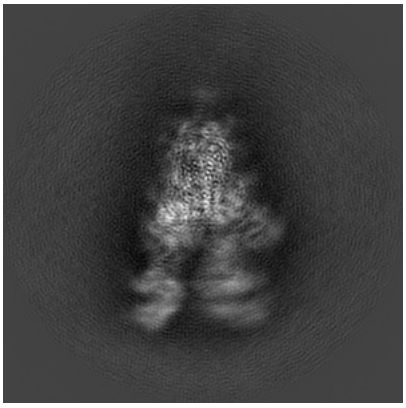
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-22893. These allow visual inspection of the internal detail of the map and identification of artifacts.

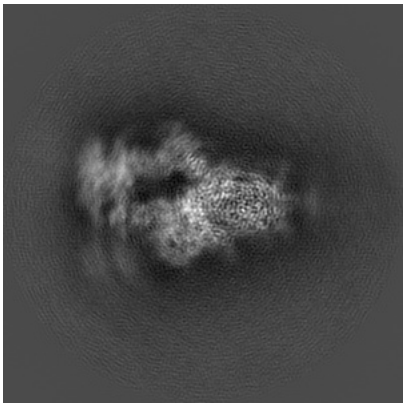
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

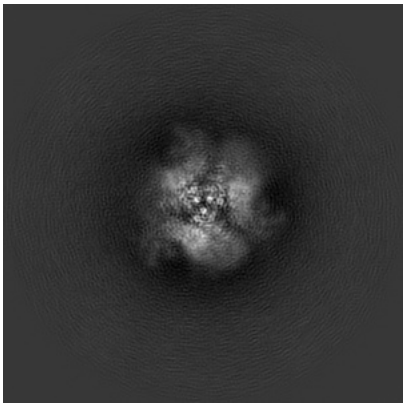
6.1.1 Primary map



X



Y



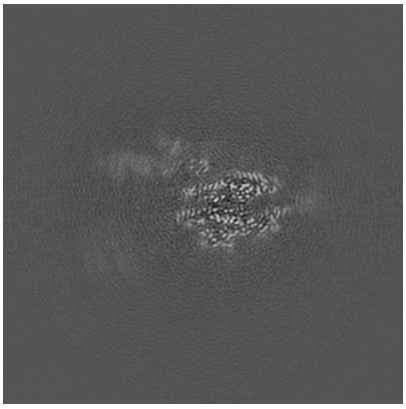
Z

The images above show the map projected in three orthogonal directions.

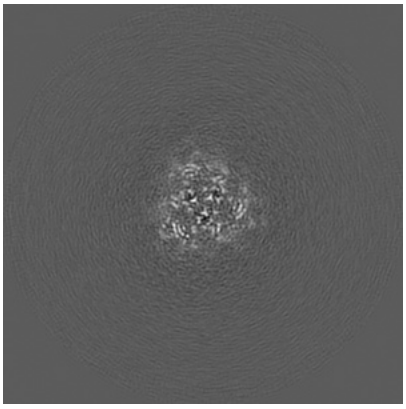
6.2 Central slices (i)

6.2.1 Primary map

X Index: 240



Y Index: 240

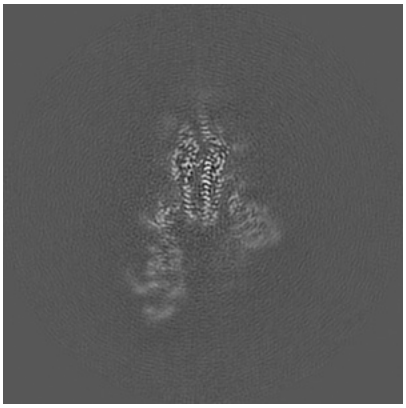


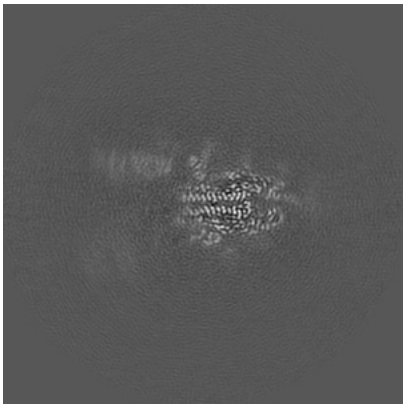
Z Index: 240

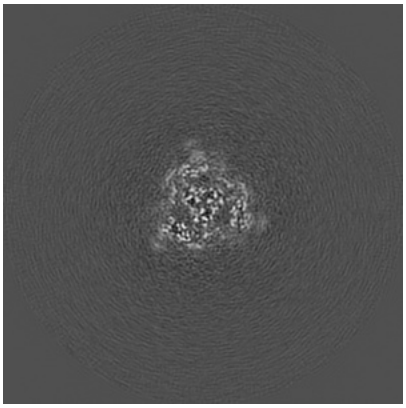
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map


X Index: 231

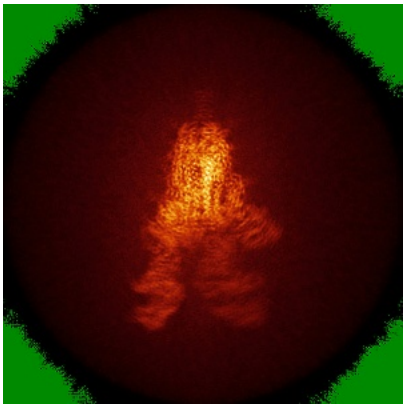

Y Index: 246

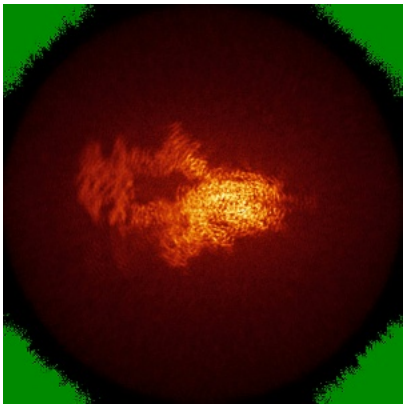

Z Index: 237

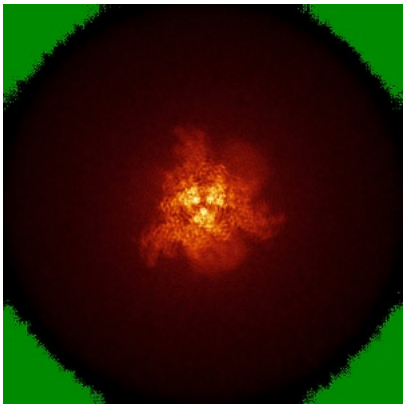
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map


X

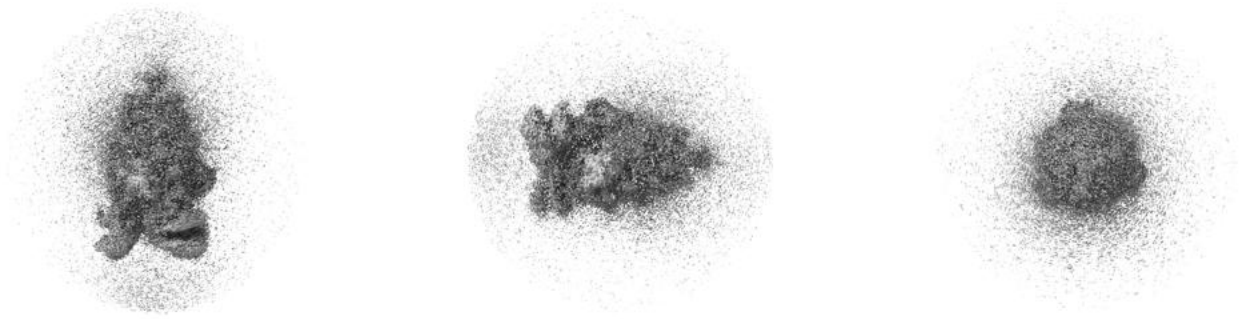

Y


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

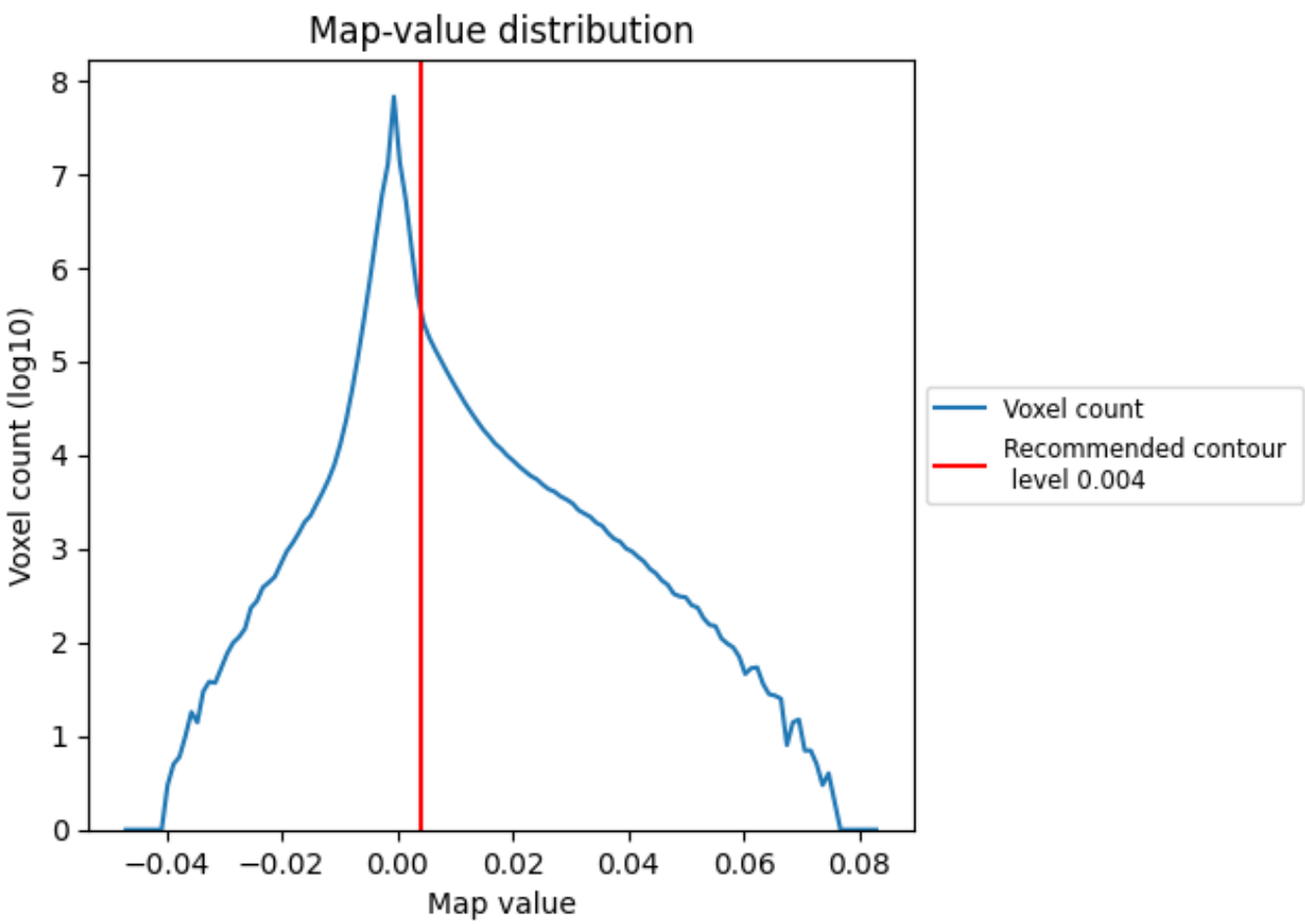
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

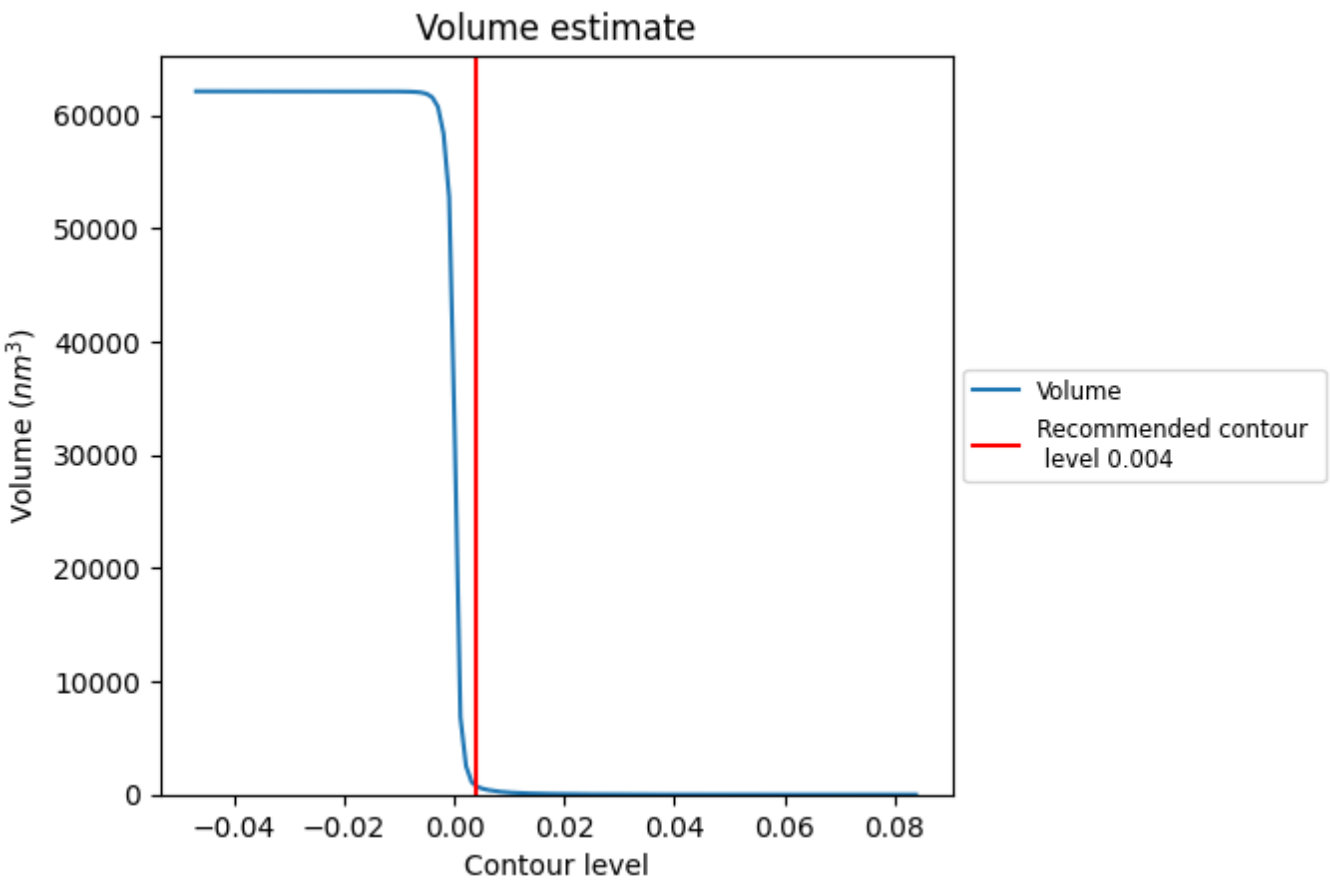
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

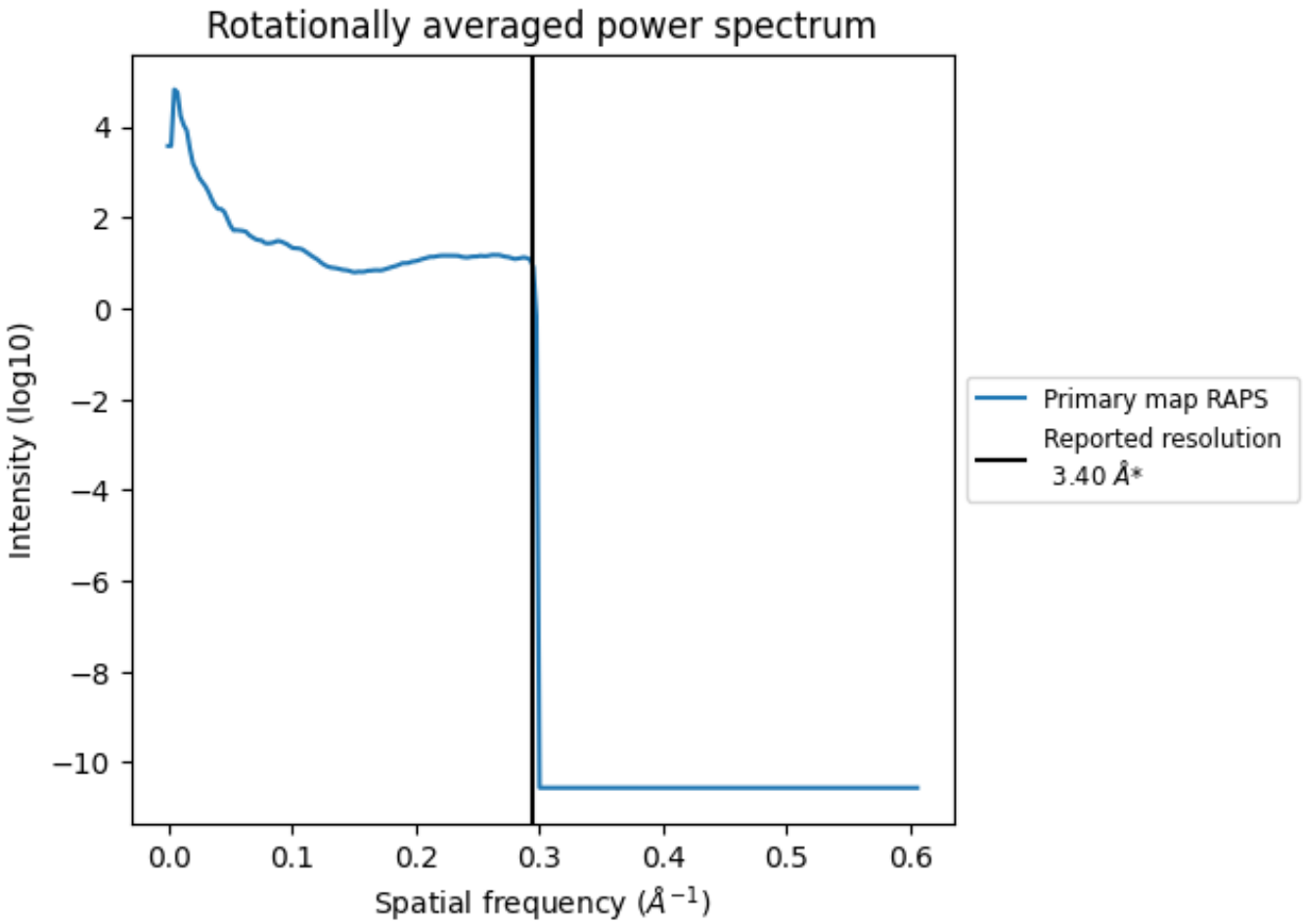
7.2 Volume estimate (i)



The volume at the recommended contour level is 752 nm^3; this corresponds to an approximate mass of 679 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8 Fourier-Shell correlation (i)

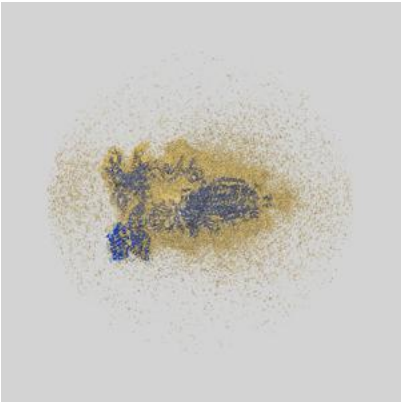
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit (i)

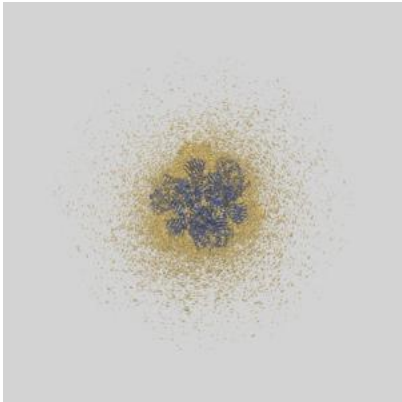
This section contains information regarding the fit between EMDB map EMD-22893 and PDB model 7KJ4. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay (i)

X



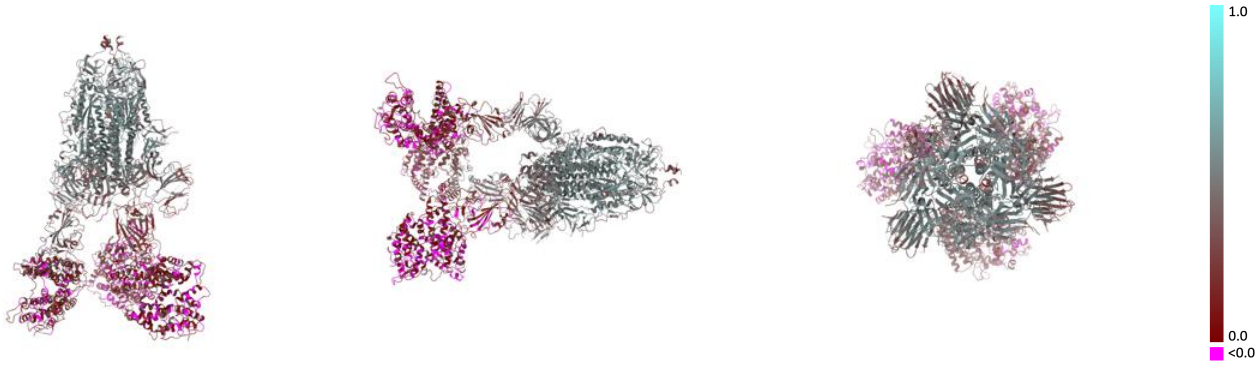
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

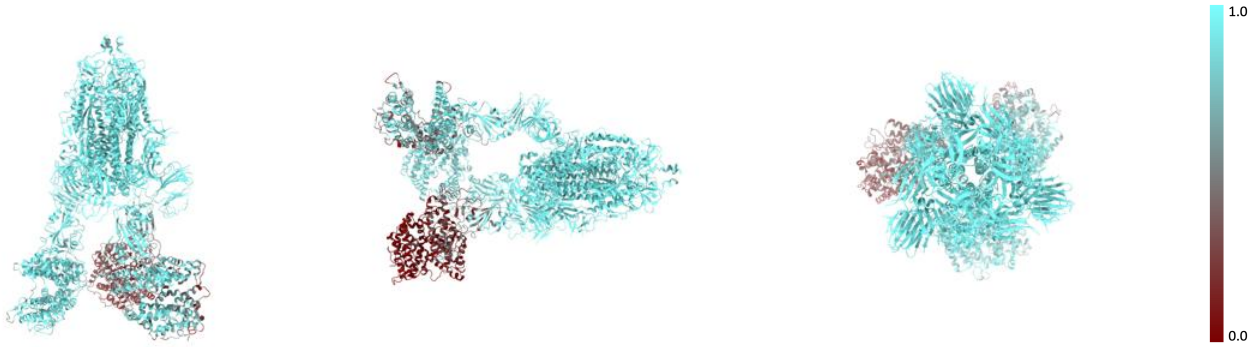
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

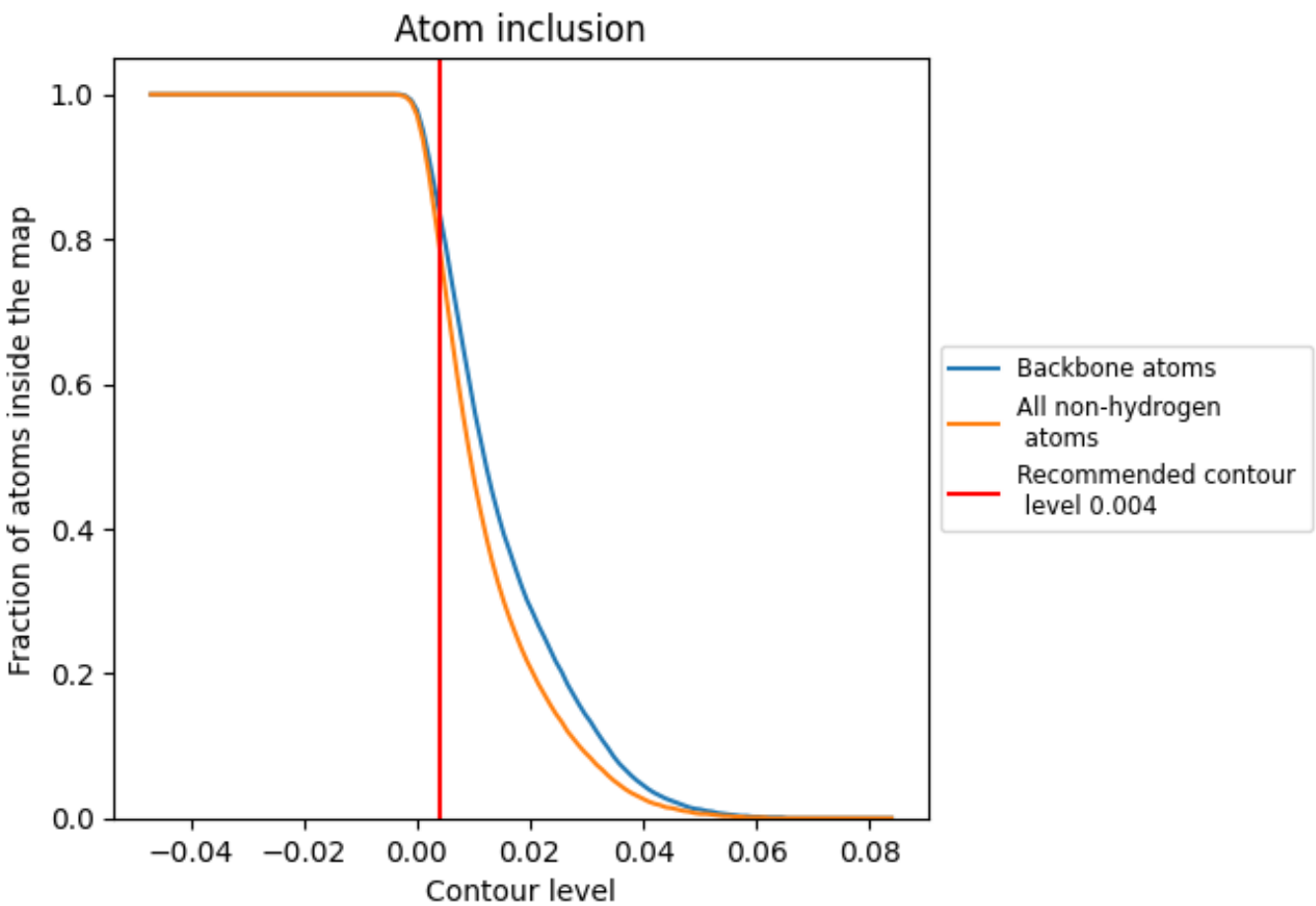
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.004).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7910	0.3070
A	0.8910	0.4130
B	0.9580	0.4480
C	0.9430	0.4150
D	0.8850	0.1760
E	0.7080	0.1120
F	0.1370	0.0770
G	1.0000	0.4500
H	0.8930	0.2660
I	0.8210	0.2360
J	0.9640	0.3730
K	0.9640	0.4090
L	0.9290	0.3810
M	1.0000	0.4550
N	0.9640	0.3800
O	0.9640	0.3830
P	0.5360	-0.0800
Q	0.6070	0.1240
R	0.5710	0.0040
S	0.2500	0.0520
T	0.7140	0.0900
U	0.2500	0.0090
V	0.3210	0.0940
W	0.5710	0.2210
X	0.1070	0.1370
Y	0.1070	-0.0960
Z	0.2140	0.1230
a	0.0360	0.0940
b	0.1430	0.1260
c	0.0000	0.0380
d	0.0710	0.2940